

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 12, 2005, 12:47:25 ; Search time 101.484 Seconds  
(without alignments)  
38.883 Million cell updates/sec

Title: US-10-657-404A-1  
Perfect score: 63  
Sequence: 1 KAEYKXKXKXKX 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues  
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.GeneSeq.23Sep04:\*  
1: GeneSeqP1980s:\*  
2: GeneSeqP1990s:\*  
3: GeneSeqP2000s:\*  
4: GeneSeqP2001s:\*  
5: GeneSeqP2002s:\*  
6: GeneSeqP2003as:\*  
7: GeneSeqP2003bs:\*  
8: GeneSeqP2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	11	2	AAW57204 Apo B bin
2	60	95.2	16	6	ABJ37574 Heparin b
3	60	95.2	20	5	AAE14542 Human apo
4	60	95.2	24	5	AAE14545 Human apo
5	60	95.2	50	2	AAW96844 Nucleic a
6	60	95.2	138	2	AAW41259 Apolipop
7	60	95.2	394	2	AAW96831 Nucleic a
8	60	95.2	2463	8	ADJ57400 Human apo
9	60	95.2	3923	8	AAV31237 Human apo
10	60	95.2	4536	2	AAW41262 Apolipop
11	60	95.2	4536	2	AAW96826 Amino aci
12	60	95.2	4560	5	AAU98981 Human pro
13	60	95.2	4561	7	ADD48677 Human pro
14	60	95.2	4563	5	AAO15893 Human apo
15	60	95.2	4563	6	ABR40253 Human a1
16	60	95.2	4563	6	ABU79140 Apolipop
17	60	95.2	4563	7	ADP43408 Apolipop
18	60	95.2	4563	8	ADH18871 Human apo
19	60	95.2	4563	8	ADH18870 Human apo
20	60	95.2	4563	8	ADH18870 Human apo
21	60	95.2	4563	8	ADH18870 Human apo
22	60	95.2	4563	8	ADH18870 Human apo
23	60	95.2	4563	8	ADH18870 Human apo
24	60	95.2	4563	8	ADH18870 Human apo
25	60	95.2	4563	8	ADH18870 Human apo

26	47	74.6	20	6	AAE33988 Human apo
27	47	74.6	20	8	ADN00545 Apolipop
28	47	74.6	20	8	ADN98185 Apolipop
29	47	74.6	43	2	AAW96874 Nucleic a
30	41.5	65.9	577	3	AAG48997 Arabidops
31	41.5	65.9	596	3	AAG48996 Arabidops
32	41.5	65.9	660	3	AAW48995 Arabidops
33	41	65.1	1213	2	AAW06086 Drosophil
34	41	65.1	1213	2	AAW25029 Trif-bind
35	41	65.1	1219	4	ABE62618 Drosophil
36	40	63.5	39	4	AAE06242 H-K2b pol
37	40	63.5	59	4	AAE06243 H-K2b pol
38	40	63.5	79	8	ADP71384 Polymex o
39	40	63.5	769	8	ADH181620 C. elegan
40	39	61.9	10	4	AAG94651 Human com
41	39	61.9	79	4	AAE06244 H-K2b pol
42	39	61.9	196	6	ABP60674 Translati
43	39	61.9	261	6	ADA21104 Human sec
44	39	61.9	328	6	ABP79068 N. gonorr
45	39	61.9	628	4	ABG18881 Novel hum

## ALIGNMENTS

RESULT 1	AAW57204 standard; peptide; 11 AA.
AAW57204	AAW57204 standard; peptide; 11 AA.
AC	AAW57204; (first entry)
DT	03-AUG-1998
DE	Apo B binding site peptide 1.
XX	Apo B; binding site; receptor; cancer; drug delivery; anticancer;
XX	growth supplement; non-natural lipid particle; low density lipoprotein;
XX	LDL; receptor component; apo B100 receptor site.
OS	Synthetic.
XX	MO9813385-A2.
XX	02-APR-1998.
PD	25-SEP-1997; 97WO-GB002610.
XX	27-SEP-1996; 96GB-00020153.
PR	(UYST ) UNIV STRATHCLYDE.
PA	Halbert GW, Owens MD, Baillie G;
XX	WPI; 1998-230637/20.
PT	Non-natural lipid particle comprising peptide binding to apo B protein
PT	receptor - useful as, e.g. vector for delivering drugs to cancer cells
XX	that express this receptor.
PS	Claim 12; Page 52; 73pp; English.
XX	The present sequence represents a specifically claimed Apo B binding site
CC	peptide which can be used as a component of a non-naturally occurring,
CC	receptor-competent low density lipoprotein (LDL) particle of the present
CC	invention. The LDL particle comprises at least 1 peptide component that
CC	has at least 1 binding site for an apo B protein receptor and at least 1
CC	lipophilic substituent. Also described in the invention are peptides
CC	containing an apo B binding sequence with at least 70% identity with
CC	sequences: KAEYKXKXKXKX (1) or TRLTRKRGUK (2), or their dimers. Non-
CC	naturally occurring, receptor-competent LDL particles are useful as: (i)
CC	drug-targeting vectors for delivering anticancer drugs to cancer cells
CC	that express an apo B protein receptor, and (ii) additives for cell
CC	culture media especially as growth supplements. Non-naturally occurring,

APP1.

CC receptor-competent LDL particles do not require the complete apo B  
CC sequence, which is large and tends to aggregate, to provide binding  
XX affinity to an apo B protein receptor  
XX  
SQ Sequence 11 AA;

Query Match 100.0%; Score 63; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KAEYKKNKRRH 11  
DB 1 KAEYKKNKRRH 11

RESULT 2  
ABJ37574  
ID ABJ37574 standard; peptide; 16 AA.  
XX  
AC ABJ37574;  
XX  
DT 10-MAY-2003 (first entry)  
XX  
DE Heparin binding peptide sequence #27.  
XX  
KW Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;  
XX cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour;  
XX rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.  
XX  
OS Unidentified.  
XX  
PN WO2003007689-A2.  
XX  
PD 30-JAN-2003.  
XX  
PF 22-JUL-2002; 2002WO-US02419.  
XX  
PR 20-JUL-2001; 2001US-0306726P.  
XX  
PA (ETHZ-) ETH ZUERICH.  
XX  
PI (UYZU-) UNIV ZURICH.  
XX  
PI Hubbell JA, Schoenmakers R, Maynard HD;  
XX  
DR WPI; 2003-300420/29.

PT Use of a ligand comprising of at least one sulfated or sulfonated amino  
PT acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic  
PT retinopathy and hypoxia.  
XX  
PS Disclosure; Fig 2; 79pp; English.  
XX  
CC The invention relates to a novel ligand for binding a target biomolecule,  
CC which comprises a peptide having at least one sulphated or sulfonated amino  
CC amino acid and at least one amino acid chosen from neutral and positively  
CC charged amino acids. The novel ligands can be used for the treatment of  
CC e.g. tumors, rheumatoid arthritis, diabetic retinopathy and hypoxia.  
CC This sequence represents a heparin binding peptide relating to the  
XX invention  
XX  
SQ Sequence 16 AA;

Query Match 95.2%; Score 60; DB 6; Length 15;  
Best Local Similarity 90.9%; Pred. No. 0.00078;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KAEYKKNKRRH 11  
DB 4 KAEYKKNKRRH 14

RESULT 3  
AAE14542

ID AAE14542 standard; peptide; 20 AA.  
XX  
AC AAE14542;  
XX  
DT 17-MAY-2002 (first entry)  
XX  
DE Human apob-100 derived peptide p63.  
XX  
KW Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis;  
XX cardiovascular disease; coronary heart disease; pre-eclampsia;  
XX non-insulin-dependent diabetes; endothelial dysfunction; human; apob-100;  
XX peptide p63.  
XX  
OS Homo sapiens.  
XX  
PN WO200206314-A2.  
XX  
PD 24-JAN-2002.  
XX  
PF 18-JUL-2001; 2001WO-GB003212.  
XX  
PR 18-JUL-2000; 2000GB-00017641.  
XX  
PA (ARKT-) ARK THERAPEUTICS LTD.  
XX  
PI Narayan O, Yla-Herttuala S;  
XX  
DR WPI; 2002-179777/23.  
XX  
PD New peptide useful in enzyme immunoassays for detecting oxidized low  
XX density lipoprotein which is a marker of coronary heart disease and other  
XX cardiovascular diseases, has affinity for oxidized low density  
XX lipoprotein.  
XX  
PS Claim 6; Page 5; 21pp; English.  
XX  
CC The invention relates to peptides having affinity for oxidized low  
XX density lipoprotein (oxLDL), in cyclised or multimeric form. The peptide  
XX is useful in an immunoassay to determine the presence, and optionally,  
XX the amount of antibodies in a sample, having affinity for oxLDL.  
XX Preferably immobilised peptide is useful for measuring the amount of  
XX autoantibodies for oxLDL in a sample, especially a serum or plasma sample  
XX from a patient for evaluating the risk of coronary heart diseases, other  
XX cardiovascular diseases, and several other disorders such as  
XX periaortitis, pre-eclampsia, non-insulin-dependent diabetes and  
XX endothelial dysfunction. The peptide of the invention is stable, can be  
XX synthesised easily without the need to isolate proteins from a patient's  
XX blood, and has a long half-life. The present sequence is human apob-100  
XX derived peptide p63 used in the invention  
XX  
SQ Sequence 20 AA;

Query Match 95.2%; Score 60; DB 5; Length 20;  
Best Local Similarity 90.9%; Pred. No. 0.00099;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KAEYKKNKRRH 11  
DB 4 KAEYKKNKRRH 14

RESULT 4  
AAE14545  
ID AAE14545 standard; peptide; 24 AA.  
XX  
AC AAE14545;  
XX  
DT 17-MAY-2002 (first entry)  
XX  
DE Human apob-100 derived peptide p244.  
XX  
KW Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis;  
XX cardiovascular disease; coronary heart disease, pre-eclampsia,  
XX

XX  
KW

KW non-insulin-dependent diabetes; endothelial dysfunction; human; apob-100;  
KW peptide p244.  
XX  
XX Homo sapiens.  
OS  
XX MO200206314-A2.  
PN  
XX 24-JAN-2002.  
XX  
XX 18-JUL-2001; 2001WO-GB003212.  
PF  
XX 18-JUL-2000; 2000GB-00017641.  
PR  
XX (ARKT-) ARK THERAPEUTICS LTD.  
PA  
XX Narvanen O, Yla-Herttuala S;  
PI  
XX WPI; 2002-179777/23.  
DR  
XX  
XX New peptide useful in enzyme immunoassays for detecting oxidized low  
PT density lipoprotein which is a marker of coronary heart disease and other  
PT cardiovascular diseases, has affinity for oxidized low density  
PT lipoprotein.  
XX  
XX Claim 7; Page 21; 21pp; English.  
PS  
XX The invention relates to peptides having affinity for oxidised low  
CC density lipoprotein (oxLDL), in cyclised or multimeric form. The peptide  
CC is useful in an immunoassay to determine the presence, and optionally,  
CC the amount of antibodies in a sample, having affinity for oxLDL.  
CC Preferably immobilised peptide is useful for measuring the amount of  
CC autoantibodies for oxLDL in a sample, especially a serum or plasma sample  
CC from a patient for evaluating the risk of coronary heart diseases, other  
CC cardiovascular diseases, and several other disorders such as  
CC periaortitis, pre-eclampsia, non-insulin-dependent diabetes and  
CC endothelial dysfunction. The peptide of the invention is stable, can be  
CC synthesised easily without the need to isolate proteins from a patient's  
CC blood, and has a long half-life. The present sequence is human apob-100  
CC derived peptide p244 used in the invention  
XX  
SQ Sequence 24 AA;  
Query Match 95.2%; Score 60; DB 5; Length 24;  
Best Local Similarity 90.9%; Pred. No. 0.0012;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KAEYKKNKGRH 11  
Db 6 KAOYKKNKGRH 16  
RESULT 5  
AAW6844  
ID AAW6844 standard; peptide; 50 AA.  
XX  
AC AAW6844;  
XX  
XX 22-APR-1999 (first entry)  
XX  
DE Nucleic acid binding domain from apob-100.  
XX  
KW Human apolipoprotein B-100; apob-100; very-low density lipoprotein; VLDL;  
KW apolipoprotein; binding; in vivo transport; nucleic acid; binding domain;  
KW nuclear localization sequence; gene therapy; cancer; cystic fibrosis;  
KW non-small cell lung carcinoma; diabetes; arteriosclerosis.  
XX  
XX Homo sapiens.  
OS  
XX W09856938-A1.  
PN  
XX 17-DEC-1998.  
PD  
XX 10-JUN-1998; 98WO-US011927.  
PF

XX  
PR 13-JUN-1997; 97US-00874807.  
PR 14-MAY-1998; 98US-00079030.  
XX  
XX (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA  
XX Guevara JG, Hoogveen RC, Moore JP;  
PI  
XX WPI; 1999-070331/06.  
DR  
XX  
XX Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -  
PT used for delivering nucleic acid to cells for gene therapy and antisense  
PT treatment.  
XX  
XX Claim 16; Page 150-151; 293pp; English.  
PS  
XX AAW6827-77 represent nucleic acid binding domains derived from human  
CC apolipoprotein B-100 (apob-100). Apob-100 is a major apoprotein component  
CC of very-low density lipoproteins (VLDL), intermediate density lipoprotein  
CC (IDL), low density lipoproteins (LDL) and lipoprotein a. The present  
CC sequence can be used in the composition of the invention. The  
CC specification describes a composition that comprises LDL and  
CC apolipoproteins for the binding and in vivo transport of nucleic acids.  
CC The composition is used to deliver nucleic acids to eukaryotic cells, in  
CC vivo or in vitro, for expressing a therapeutic polypeptide or antisense  
CC molecule (or ribozyme). Specifically they are used for gene therapy of  
CC cancers (particularly non-small cell lung carcinoma), diabetes, cystic  
CC fibrosis and arteriosclerosis  
XX  
SQ Sequence 50 AA;  
Query Match 95.2%; Score 60; DB 2; Length 50;  
Best Local Similarity 90.9%; Pred. No. 0.0026;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KAEYKKNKGRH 11  
Db 2 KAOYKKNKGRH 12  
RESULT 6  
AAW41259  
ID AAW41259 standard; peptide; 138 AA.  
XX  
AC AAW41259;  
XX  
XX 19-MAY-1998 (first entry)  
XX  
DE Apolipoprotein B-100 fragment.  
XX  
XX Anti-coagulant; apolipoprotein B-100; apob-100; metastatic spread;  
KW thromboplastin-mediated process; cancer; inhibitor; blood coagulation;  
KW angiogenesis; cellular differentiation; apoptosis; KRAD-14;  
KW prothrombinase complex.  
XX  
XX Synthetic.  
OS  
XX Homo sapiens.  
OS  
XX W09743311-A1.  
PN  
XX 20-NOV-1997.  
PD  
XX 09-MAY-1997; 97WO-GB001255.  
PF  
XX 09-MAY-1996; 96GB-00009702.  
PR  
XX (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.  
PA  
XX Bruckdorfer KR, Ectelate C;  
PI  
XX WPI; 1998-008798/01.  
DR  
XX Peptide fragments of apo:lipoprotein B-100 with anticoagulant activity -  
PT

PT used for treating or preventing coagulation, inhibiting angiogenesis,  
 PT cell differentiation and apoptosis.  
 PS Claim 2; Page 8; 60pp; English.

CC This sequence is an example of the peptide of the invention. It has the  
 CC formula (1), or their variants with one or more internal deletions,  
 CC insertions or substitutions, while retaining anti-coagulant properties,  
 CC apolipoprotein B-100 (apob-100). 21-KAQ-XI-KKKKHS-X2-1-42 (I) X1 = S or  
 CC Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids  
 CC (aa); Z2 = the C terminus of the peptide, a terminal amide group or 1-77  
 CC separate or sequential treatment of cancer, particularly to prevent  
 CC metastatic spread; they are also used to inhibit thromboplastic-mediated  
 CC processes, specifically to prevent or reduce blood coagulation (e.g.  
 CC inhibit angiogenesis, cellular differentiation or apoptosis, stroke etc.) and to  
 CC which is active as such or as part of a 98-aa peptide, RXAD-14, and to  
 CC activation of the prothrombinase complex, and prevents activation of  
 CC factor VII on the surface of thromboplastin and of platelets by thrombin.  
 CC It binds to the residues 58-66 of thromboplastin and of platelets by thrombin.  
 CC smaller than apob-100, they act more quickly  
 XX Sequence 138 AA;

Query Match Best Local Similarity 95.2%; Score 60; DB 2; Length 138;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 KAEYKKNKRRH 11  
 ||:|||||  
 48 KAYKKKKNRRH 58

RESULT 7  
 AAW96831 standard; peptide; 394 AA.  
 XX AAW96831;  
 AC AAW96831;  
 DT 22-APR-1999 (first entry)

XX Nucleic acid binding domain from apob-100, residues 2930-3324.  
 XX Human apolipoprotein B-100; apob-100; Very-low density lipoprotein; VLDL;  
 KW apolipoprotein; binding; in vivo transport; nucleic acid; binding domain;  
 KW nuclear localisation sequence; gene therapy; cancer; cystic fibrosis;  
 XX non-small cell lung carcinoma; diabetes; arteriosclerosis.  
 OS Homo sapiens.

XX MO9856938-A1.  
 XX 17-DEC-1998.  
 PD 10-JUN-1998; 98MO-US011927.  
 PF 13-JUN-1997; 97US-00874807.  
 PR 14-MAY-1998; 98US-00079030.  
 XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Guevara JG, Hoogveen RC, Moore JP;  
 DR WPI; 1999-070331/06.  
 XX Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -  
 PT treatment.  
 PT used for delivering nucleic acid to cells for gene therapy and antisense  
 XX Claim 16; Page 144-145; 293pp; English.  
 CC AAW96827-77 represent nucleic acid binding domains derived from human

CC apolipoprotein B-100 (apob-100). Apob-100 is a major apoprotein component  
 CC of very-low density lipoproteins (VLDL), intermediate density lipoprotein  
 CC (IDL), low density lipoproteins (LDL) and lipoprotein a. The present  
 CC sequence can be used in the composition of the invention. The present  
 CC specification describes a composition that comprises LDL and  
 CC apolipoproteins for the binding and in vivo transport of nucleic acids.  
 CC The composition is used to deliver nucleic acids to eukaryotic cells, in  
 CC vivo or in vitro, for expressing a therapeutic polypeptide or antisense  
 CC molecule (or ribozyme). Specifically they are used for gene therapy of  
 CC cancers (particularly non-small cell lung carcinoma), diabetes, cystic  
 CC fibrosis and arteriosclerosis  
 XX Sequence 394 AA;

Query Match Best Local Similarity 95.2%; Score 60; DB 2; Length 394;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 KAEYKKNKRRH 11  
 ||:|||||  
 218 KAYKKKKNRRH 228

RESULT 8  
 ADJ57400 standard; protein; 2463 AA.  
 XX ADJ57400;  
 AC ADJ57400;  
 DT 06-MAY-2004 (first entry)

XX Human apolipoprotein B, marker for hepatocellular carcinoma.  
 DE Hepatocellular carcinoma; marker; human; apolipoprotein B; diagnosis.  
 KW Hepatocellular carcinoma; marker; human; apolipoprotein B; diagnosis.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 PN MO2004005466-A2.  
 PD 15-JAN-2004.

XX 03-JUL-2003; 2003MO-US020841.  
 PF 03-JUL-2002; 2002US-0393982P.  
 PR (ILLU-) ILLUMIGEN BIOSCIENCES INC.  
 XX Katze M, Bumgarner R, Smit M, Rosenberg G;  
 PI WPI; 2004-142977/14.  
 DR GENBANK; NP\_000375.

XX Detecting hepatocellular carcinoma (HCC) in mammals comprises obtaining  
 PT and assaying a biological sample to quantify a cell-associated or a non-  
 PT cell-associated HCC-related protein and comparing the quantity to a  
 PT control level.  
 XX Disclosure; SEQ ID NO 4; 48pp; English.

XX The present sequence is that of human apolipoprotein B. This non-cell  
 CC associated protein is one of a set of proteins characterized as  
 CC diagnostic targets for hepatocellular carcinoma (HCC). Such proteins are  
 CC the products of genes identified by expression microarray analysis of  
 CC being specifically up-regulated in HCC (HCV) infected patients with HCC as  
 CC infected cirrhotic non-tumour tissue and normal liver. The invention  
 CC relates to the detection of HCC by assaying patient samples such as  
 CC tissue, plasma, serum, etc. for the presence and level of specific HCC  
 CC related proteins. A finding of elevated levels of one or more of these  
 CC proteins in a patient sample indicates that the patient has HCC. Methods  
 CC for the diagnosis of HCC are provided, as well as improved assay methods  
 CC and scanning methods that employ non-cell-associated and cell-associated  
 CC HCC-related proteins.

XX SQ Sequence 2463 AA;  
Query Match 95.2%; Score 60; DB 8; Length 2463;  
Best Local Similarity 90.9%; Pred. No. 0.16;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KAEYKKNKRRH 11  
||:|||||  
DB 1074 KAQYKKNKRRH 1084  
RESULT 9  
ID AAY31237 standard; protein; 3923 AA.  
AC AAY31237;  
XX AAY31237;  
XX 08-NOV-1999 (first entry)  
XX  
XX Human Apo B protein fragment.  
DE  
XX Apo E; Apo B; hyperlipidemia; human; treatment; hepatocyte; apoprotein;  
XX Apo A1; low density lipoprotein; LDL; blood; therapy; atherosclerosis;  
XX high density lipoprotein; HDL; cholesterol; coronary heart disease;  
XX Alzheimer's disease; hypobetalipoproteinemia; dysbetalipoproteinemia.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH 1..3923  
FT Protein /label= Apo B  
FT /note= "Partial sequence, no start codon given"  
FT  
XX WO9940789-A1.  
XX 19-AUG-1999.  
XX 28-AUG-1998; 98WO-US017908.  
XX 12-FEB-1998; 98US-0074497P.  
XX 30-JUN-1998; 98US-00108006.  
XX  
XX (MINU ) UNIV MINNESOTA.  
XX (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.  
XX  
XX Steer CJ, Kren BT, Bandyopadhyay PT, Roy-Chowdhury J;  
XX WPI, 1999-527333/44.  
XX N-PSDB; AA209525.  
XX  
XX Mutating apolipoprotein genes in hepatocytes to control cholesterol  
XX levels, e.g. for treating or preventing hyperlipidemia, particularly  
XX atherosclerosis.  
XX  
XX Claim 4; Page 75-83; 106pp; English.  
XX  
XX This invention describes a novel method for the genetic treatment of  
XX hyperlipidemia by altering genes, in hepatocytes, for apoprotein (apo) B,  
XX E or A1. Low density lipoprotein (LDL) levels in the blood are reduced by  
XX altering an apo B gene (II) in a hepatocyte. The invention describes a  
XX method for the therapeutic and/or prophylactic method involving altering  
XX an apo E gene in hepatocytes by introducing the mutations Arg12Cys,  
XX Arg158Cys or Cys158Arg and a method for ameliorating atherosclerosis by  
XX altering the apo A1 gene in a hepatocyte so that the altered protein can  
XX dimerize. Altering expression of apo genes regulates levels of high and  
XX low density lipoprotein cholesterol. Altering expression of apo B, E and  
XX A1 genes is used to treat or prevent atherosclerosis, coronary heart  
XX disease, Alzheimer's disease, hypobetalipoproteinemia, and  
XX dysbetalipoproteinemia. This sequence represents a fragment of the human  
XX Apo B protein described in the method of the invention  
SQ Sequence 3923 AA;

Query Match 95.2%; Score 60; DB 2; Length 3923;  
Best Local Similarity 90.9%; Pred. No. 0.26;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KAEYKKNKRRH 11  
||:|||||  
DB 2534 KAQYKKNKRRH 2544  
RESULT 10  
ID AAM41262 standard; peptide; 4536 AA.  
AC AAM41262;  
XX AAM41262;  
XX 19-MAY-1998 (first entry)  
XX  
XX Apolipoprotein B-100.  
DE  
XX Anti-coagulant; apolipoprotein B-100; apob-100; metastatic spread;  
XX thromboplastin-mediated process; cancer; inhibitor; blood coagulation;  
XX angiogenesis; cellular differentiation; apoptosis; KRAD-14;  
XX prothrombinase complex.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9743311-A1.  
XX 20-NOV-1997.  
XX  
XX 09-MAY-1997; 97WO-GB001255.  
XX  
XX 09-MAY-1996; 96GB-00009702.  
XX  
XX (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.  
XX  
XX Bruckdorfer KR, Etelate C;  
XX WPI, 1998-008798/01.  
XX  
XX Peptide fragments of apo:liipo:protein B-100 with anticoagulant activity -  
XX used for treating or preventing coagulation, inhibiting angiogenesis,  
XX cell differentiation and apoptosis.  
XX  
XX Disclosure; Page 42-47; 60pp; English.  
XX  
XX This sequence represents the human apolipoprotein B-100 (apob-100).  
XX Fragments of this sequence can be used in the peptide of the invention,  
XX which has the formula (I), or their variants with one or more internal  
XX deletions, insertions or substitutions, while retaining anti-coagulant  
XX properties of apolipoprotein B-100 (apob-100). Z1-KAQ-X1-KKNKRRHS-X2-T-Z2  
XX (I); X1 = S or Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-  
XX 47 amino acids (aa); Z2 = the C terminus of the peptide, a terminal amide  
XX group or 1-77 aa. Compositions containing the peptide are used for  
XX simultaneous, separate or sequential treatment of cancer, particularly to  
XX prevent metastatic spread. They are also used to inhibit thromboplastin-  
XX mediated processes, specifically to prevent or reduce blood coagulation  
XX (e.g. during or after surgery or in cases of heart attack, stroke etc.)  
XX and to inhibit angiogenesis, cellular differentiation or apoptosis. KRAD-  
XX 14, which is active as such or as part of a 98-aa peptide, inhibits  
XX activation of the prothrombinase complex; and prevents activation of  
XX factor VII on the surface of thromboplastin and of platelets by thrombin.  
XX It binds to the residues 58-66 of thromboplastin. Since (I) are much  
XX smaller than apob-100, they act more quickly  
SQ Sequence 4536 AA;  
Query Match 95.2%; Score 60; DB 2; Length 4536;  
Best Local Similarity 90.9%; Pred. No. 0.31;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KAEYKKNKRRH 11

Db 3147 KAQYKKNKRRH 3157

## RESULT 11

AAW96826 ID AAW96826 standard; protein; 4536 AA.

AC AAW96826; XX 22-APR-1999 (first entry)

DE Amino acid sequence of human apolipoprotein B-100 (apoB-100).

XX Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL;  
XX apolipoprotein; binding; in vivo transport; nucleic acid; binding domain;  
XX nuclear localization sequence; gene therapy; cancer; cystic fibrosis;  
XX non-small cell lung carcinoma; diabetes; arteriosclerosis.  
OS Homo sapiens.

XX WO9856938-A1.

XX 17-DEC-1998.

XX 10-JUN-1998; 98WO-US011927.

XX 13-JUN-1997; 97US-00874807.

XX 14-MAY-1998; 98US-00079030.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Guevara JG, Hoogveen RC, Moore JP;  
XX WPI; 1999-070331/06.

XX Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -  
XX used for delivering nucleic acid to cells for gene therapy and antisense  
XX treatment.

XX Disclosure; Fig 1A-C; 293pp; English.

XX The present sequence represents human apolipoprotein B-100 (apoB-100).  
XX apoB-100 is a major apolipoprotein component of very-low density lipoproteins  
XX (VLDL), intermediate density lipoprotein (IDL), low density lipoproteins  
XX (LDL), and lipoprotein a. The specification describes a composition that  
XX comprises LDL and apolipoproteins for the binding and in vivo transport  
XX of nucleic acids. Binding domains (see AAW96827-77) and nuclear  
XX localization sequences (see AAW96878-97) for use in the composition can  
XX be derived from the present sequence. The composition is used to deliver  
XX therapeutic acids to eukaryotic cells, in vivo or in vitro, for expressing a  
XX therapeutic polypeptide or antisense molecule (or ribozyme). Specifically  
XX they are used for gene therapy of cancers (particularly non-small cell  
XX lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis

SO Sequence 4536 AA;

Query Match Best Local Similarity 95.2%; Score 60; DB 2; Length 4536;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11  
Db 3147 KAQYKKNKRRH 3157

## RESULT 12

AAU98981

XX AAU98981 standard; protein; 4560 AA.

AC AAU98981; XX

DT 05-NOV-2002 (first entry)

XX Human apolipoprotein B100 (apoB100).  
XX Human; low density lipoprotein receptor; LDLR; apolipoprotein E; apoE;  
XX virus-lipoprotein complex; apolipoprotein B100; apoB100; VSV;  
XX Flaviviridae virus; vesicular stomatitis virus; cholesterol metabolism.  
OS Homo sapiens.

XX Key

XX Region Location/Qualifiers  
XX Region 2835..4189  
XX Region /note= "Epiptope region; specifically claimed in claim 11"  
XX Region 2980..3084  
XX Region /note= "Epiptope region; specifically claimed in claim 11"

XX WO200248388-A2.

XX 20-JUN-2002.

XX 24-OCT-2001; 2001WO-US050701.

XX 25-OCT-2000; 2000US-0243594P.

XX (AGNE/) AGNELLO V.

XX Agnello V;

XX WPI; 2002-583528/62.

XX Inhibiting infection of cell by virus capable of forming complex with  
XX lipoprotein, by preventing formation or altering conformation of complex,  
XX or blocking cell receptor for the complex using antibody to receptor.  
XX Claim 11, Page 44-47; 49pp; English.

XX The invention relates to a method of inhibiting infection of a cell by  
XX virus capable of forming a complex with lipoprotein. The method comprises  
XX preventing formation of and altering conformation of the complex to  
XX prevent its interaction with cell receptor (CR), blocking CR using  
XX antibody to receptor or binding of lipoprotein complex to CR using  
XX soluble lipoprotein receptor, or downregulating low density lipoprotein  
XX receptor activity of cells. In this method, inhibition of infection  
XX involves preventing formation of a complex between the lipoprotein and  
XX virus, and dissociating the virus and lipoprotein, or by introducing  
XX lipase to the cell, which is capable of inducing a conformational change  
XX of a virus-lipoprotein complex. Alternatively, the method involves  
XX introducing anti-low density lipoprotein (LDL) receptor antibody (anti-  
XX LDLR) which binds to an epitope included in the ligand binding domain of  
XX the receptor, or anti-apolipoprotein (apo)B100 antibody which binds to an  
XX epitope included in the LDL-receptor binding domain of apoB100, or anti-  
XX apoB antibody which binds to an epitope included in LDL receptor binding  
XX domain of apoB. The method also involves introducing a peptide comprising  
XX where the peptide fragment binds to the receptor binding domain of LDL  
XX or apoB, or downregulating lipoprotein receptor activity of apoB.  
XX The method is useful for inhibiting or preventing infection of a cell by  
XX viruses such as Flaviviridae virus, vesicular stomatitis virus or other  
XX inhibition of infection occurs without harmful effects on cholesterol  
XX metabolism. The present sequence represents apolipoprotein B100 (apoB100)

SO Sequence 4560 AA;

Query Match Best Local Similarity 95.2%; Score 60; DB 5; Length 4560;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11  
Db 3171 KAQYKKNKRRH 3181

## RESULT 13

ADD48677  
 ID ADD48677 standard; protein; 4561 AA.  
 XX  
 AC ADD48677;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human Protein X04714, SEQ ID NO 14384.  
 XX  
 KM Human; pain; neuronal tissue; gene therapy;  
 KM spinal segmental nerve injury; chronic constriction injury; CCI;  
 KM spared nerve injury; SNI; Chung.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2003016475-A2.  
 PD  
 PD 27-FEB-2003.  
 XX  
 PF 14-AUG-2002; 2002MO-US025765.  
 XX  
 PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX  
 PI Woolf C, D'Urso D, Befort K, Costigan M;  
 XX  
 DR WPI; 2003-268312/26.  
 DR GENBANK; X04714.  
 XX  
 PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX  
 PS Claim 1; Page; 1017pp; English.  
 XX  
 CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a human protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX  
 SO Sequence 4561 AA;

Query Match 95.2%; Score 60; DB 7; Length 4561;  
 Best Local Similarity 90.9%; Pred. No. 0.31;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 KAEYKKNKGRH 11

DB 3171 KAEYKKNKGRH 3181  
 ||:|||||  
 RESULT 14  
 ID AAO15893  
 XX AAO15893 standard; protein; 4563 AA.  
 XX  
 AC AAO15893;  
 XX  
 DT 30-JAN-2003 (first entry)  
 XX  
 DE Human apolipoprotein B (APOB).  
 XX  
 KM Human; gene therapy; single nucleotide polymorphism; SNP;  
 KM cytochrome C oxidase subunit VIb; COX6B; high serum cholesterol; GPI-1;  
 KM N-acetylglucosaminyl transferase component; cardiovascular disease; HDL;  
 KM glycosylphosphatidylinositol-1; low serum high density lipoprotein.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200272604-A2.  
 PD  
 PD 19-SEP-2002.  
 XX  
 PF 05-MAR-2002; 2002MO-US006728.  
 XX  
 PR 09-MAR-2001; 2001US-00802640.  
 XX  
 PA (SEQU-) SEQUENOM INC.  
 PA  
 PI Braun A, Bansal A, Kiehn PW;  
 XX  
 DR WPI; 2002-750478/81.  
 DR N-PSDB; ABT13015.  
 XX  
 PT Detecting the presence or absence of an allelic variant of a polymorphic  
 PT region of COX6B and/or GPI-1 gene, useful for detecting a predisposition  
 PT to high serum cholesterol, low serum HDL and cardiovascular disease.  
 XX  
 PS Disclosure; Page 158-168; 199pp; English.  
 XX  
 CC The invention comprises methods of detecting the presence or absence of  
 CC at least one allelic variant of a polymorphic region of a gene associated  
 CC with cardiovascular disease. The invention specifically relates to  
 CC detecting the region of a cytochrome C oxidase subunit VIb (COX6B) gene  
 CC that is associated with high serum cholesterol, or the region of the N-  
 CC acetylglucosaminyl transferase component glycosylphosphatidylinositol-1  
 CC (GPI-1) gene that is associated with low serum high density lipoprotein  
 CC (HDL). The methods of the invention are useful for detecting a  
 CC predisposition to high serum cholesterol, low serum HDL and  
 CC cardiovascular disease. The methods are also useful for elucidating  
 CC pathological pathways, developing diagnostic assays and new drug  
 CC therapies for such disorders. The present amino acid sequence represents  
 CC a human protein that is associated with high serum cholesterol, low serum  
 CC HDL and/or cardiovascular disease  
 CC  
 XX  
 SO Sequence 4563 AA;

Query Match 95.2%; Score 60; DB 5; Length 4563;  
 Best Local Similarity 90.9%; Pred. No. 0.31;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 KAEYKKNKGRH 11  
 ||:|||||  
 DB 3174 KAEYKKNKGRH 3184  
 ||:|||||  
 RESULT 15  
 ID ABR40253  
 XX ABR40253 standard; protein; 4563 AA.  
 XX  
 AC ABR40253;  
 XX

Search completed: January 12, 2005, 13:25:39  
Job time : 103.484 secs

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XX 20-JUN-2003 (first entry)
DT
XX
DE Human alipoprotein B.
XX
KW Human; alipoprotein B; Apob; antilipemic; antiarteriosclerotic;
KW antidiabetic; anorectic; cardiovascular; gene therapy; lipid metabolism;
KW cholesterol metabolism; atherosclerosis; hyperlipidaemia; diabetes;
KW type 2 diabetes; obesity; atherosclerosis; cardiovascular disease;
KW glucose.
XX
OS Homo sapiens.
XX
PN WO2003011887-A2.
XX
PD 13-FEB-2003.
XX
PF 30-JUL-2002; 2002MO-US024247.
XX
PR 01-AUG-2001; 2001US-00920033.
PR 30-APR-2002; 2002US-00135985.
PR 15-MAY-2002; 2002US-00147196.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Crooke RM, Graham MJ;
XX
DR WPI; 2003-268105/26.
DR N-PSDB; ACC62114.
XX
PT New antisense oligonucleotides for modulating apolipoprotein B,
PT especially for preventing or treating atherosclerosis, hyperlipidemia or
PT diabetes, or for modulating glucose, cholesterol, lipoprotein or
PT triglyceride levels.
XX
PS Disclosure; Page 118-138; 160pp; English.
XX
CC The invention relates to a novel compound that is 8-50 nucleotides in
CC length that is targeted to a nucleic acid molecule encoding
CC apolipoprotein B (ApoB), and specifically hybridises with and inhibits
CC the expression of a nucleic acid molecule encoding ApoB; or which
CC specifically hybridises with at least an 8-nucleotide portion of an
CC active site on a nucleic acid molecule encoding ApoB. A compound of the
CC invention has antilipemic, antiarteriosclerotic, antidiabetic,
CC anorectic, and cardiovascular activity. The compound may have a use in
CC gene therapy. The antisense oligonucleotide is useful for treating an
CC animal having a disease or conditions associated with ApoB, e.g. a
CC condition involving abnormal lipid metabolism, a condition involving an
CC abnormal cholesterol metabolism, atherosclerosis, or a condition
CC involving an abnormal metabolic condition (e.g. hyperlipidaemia, diabetes
CC (specifically Type 2 diabetes), obesity, atherosclerosis, diabetes
CC cardiovascular disease). The new compound or the antisense
CC oligonucleotide is also useful for modulating glucose levels
CC (particularly plasma or serum glucose levels) in a human or diabetic
CC animal, or for modulating serum cholesterol levels, lipoprotein levels
CC (specifically VLDL, HDL or LDL) or serum triglyceride levels,
CC particularly in a human. The antisense compound is also useful for
CC preventing or delaying the onset of a disease or condition associated
CC with ApoB, or the onset of an increase in glucose levels in the animal or
CC human. The present sequence is used in the exemplification of the
CC invention
XX
SQ Sequence 4563 AA;

```

Query Match 95.2%; Score 60; DB 6; Length 4563;  
Best Local Similarity 90.9%; Pred. No. 0.31;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11  
||:|||||||  
||:|||||||  
Db 3174 KAEYKKNKRRH 3184

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 12, 2005, 13:14:21 ; Search time 25.9032 Seconds  
(without alignments)  
28.162 Million cell updates/sec

Title: US-10-657-404a-1  
Perfect score: 63  
Sequence: 1 KAEYKKNKRRH 11

Scoring table:  
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Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/aa/5A.COMB.pep:\*  
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4: /cgn2\_6/ptodata/1/aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/aa/6B.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/aa/6B.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	100.0	11	US-09-269-533A-1	Sequence 1, Appli
2	60	95.2	14	US-09-180-422B-19	Sequence 19, Appli
3	60	95.2	50	US-09-079-030-97	Sequence 97, Appli
4	60	95.2	138	US-09-180-422B-12	Sequence 12, Appli
5	60	95.2	394	US-09-079-030-83	Sequence 83, Appli
6	60	95.2	840	US-09-079-030-214	Sequence 214, Appli
7	60	95.2	4536	US-09-180-422B-27	Sequence 27, Appli
8	60	95.2	4536	US-09-079-030-1	Sequence 1, Appli
9	60	95.2	4563	US-09-108-006C-1	Sequence 1, Appli
10	60	95.2	4563	US-09-538-092-842	Sequence 842, App
11	52	82.5	12	US-09-180-422B-9	Sequence 9, Appli
12	52	82.5	13	US-09-180-422B-11	Sequence 11, Appli
13	52	82.5	14	US-09-180-422B-1	Sequence 1, Appli
14	52	82.5	18	US-09-079-030-204	Sequence 204, Appli
15	51	81.0	14	US-09-180-422B-18	Sequence 18, Appli
16	48	76.2	773	US-09-079-030-215	Sequence 215, App
17	47	74.6	10	US-09-180-422B-6	Sequence 6, Appli
18	47	74.6	11	US-09-180-422B-8	Sequence 8, Appli
19	47	74.6	12	US-09-180-422B-10	Sequence 10, Appli
20	47	74.6	43	US-09-079-030-164	Sequence 164, App
21	43	68.3	9	US-09-180-422B-5	Sequence 5, Appli
22	43	68.3	10	US-09-180-422B-7	Sequence 7, Appli
23	43	68.3	785	US-09-079-030-216	Sequence 216, App
24	42	66.7	269	US-09-270-767-37552	Sequence 37552, A
25	42	66.7	269	US-09-270-767-52769	Sequence 52769, A
26	41	65.1	1213	US-08-188-582-20	Sequence 20, Appli
27	41	65.1	1213	US-08-646-715-20	Sequence 20, Appli

ALIGNMENTS

28	39	61.9	9	4	US-09-180-422B-4	Sequence 4, Appli
29	38	60.3	215	3	US-09-134-001C-3249	Sequence 3249, Ap
30	38	60.3	308	4	US-09-248-796A-19781	Sequence 19781, A
31	38	60.3	345	4	US-09-198-452A-89	Sequence 89, Appli
32	38	60.3	491	4	US-09-248-796A-19540	Sequence 19540, A
33	37	58.7	141	4	US-09-328-352-7100	Sequence 7100, Ap
34	37	58.7	156	4	US-09-889-463A-8	Sequence 8, Appli
35	37	58.7	207	4	US-09-270-767-61968	Sequence 61968, A
36	37	58.7	208	4	US-09-270-767-60040	Sequence 60040, A
37	37	58.7	340	4	US-09-270-767-43111	Sequence 43111, A
38	37	58.7	410	4	US-09-270-767-44592	Sequence 44592, A
39	37	58.7	598	4	US-09-538-092-1083	Sequence 1083, Ap
40	37	58.7	601	4	US-09-252-991A-23280	Sequence 23280, A
41	37	58.7	601	4	US-09-889-463A-10	Sequence 10, Appli
42	37	58.7	913	1	US-08-220-151-6	Sequence 6, Appli
43	37	58.7	913	1	US-08-413-118-6	Sequence 6, Appli
44	37	58.7	913	3	US-08-473-446-6	Sequence 6, Appli
45	37	58.7	913	3	US-09-232-468A-2	Sequence 2, Appli

*APPL:CONF*

RESULT 1  
US-09-269-533A-1  
Sequence 1, Application US/09269533A  
Patent No. 6670452  
GENERAL INFORMATION:  
APPLICANT: University of Strathclyde  
APPLICANT: Halbert, Gavin  
APPLICANT: Owens, Moira  
APPLICANT: Baillie, George  
TITLE OF INVENTION: No. 6670452-Naturally Occurring Lipoprotein Particle  
FILE REFERENCE: P07885US  
CURRENT APPLICATION NUMBER: US/09/269, 533A  
CURRENT FILING DATE: 1999-06-01  
PRIOR APPLICATION NUMBER: PCT/GB97/02610  
PRIOR FILING DATE: 1997-09-25  
PRIOR APPLICATION NUMBER: GB 9620153.8  
PRIOR FILING DATE: 1996-09-27  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: ( )  
OTHER INFORMATION: Apo B binding site sequence  
US-09-269-533A-1  
Query Match 100.0%; Score 63; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00013;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 KAEYKKNKRRH 11  
Db 1 KAEYKKNKRRH 11  
RESULT 2  
US-09-180-422B-19  
Sequence 19, Application US/09180422B  
Patent No. 6444644  
GENERAL INFORMATION:  
APPLICANT: BRUCKDORFER, KARL R  
APPLICANT: ETTREICH, CAMILLE  
TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED FROM APOLIPOPROTEIN B-100  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE, P.C.

us-10-657-404a-1.ra1

STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/180,422B  
FILING DATE: 07-Dec-1998  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36663  
REFERENCE/DOCKET NUMBER: 117-268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164100  
TELEFAX: 7038164000  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
Query Match  
Best Local Similarity 95.2%; Score 60; DB 4; Length 14;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KAEYKKNKRRH 11  
Db 1 KAEYKKNKRRH 11  
1 KAEYKKNKRRH 11

RESULT 3  
US-09-079-030-97  
Sequence 97; Application US/09079030  
Patent No. 6635623  
GENERAL INFORMATION:  
APPLICANT: Guevera, Jr., Juan G.  
APPLICANT: Hoogveen, Ron C.  
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY  
NUMBER OF SEQUENCES: 229  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,030  
FILING DATE: Concurrently Herewith  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMillian, Nabeela R.  
REGISTRATION NUMBER: P-43,363  
REFERENCE/DOCKET NUMBER: ARA0-003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 97:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-09-079-030-97  
Query Match  
Best Local Similarity 95.2%; Score 60; DB 4; Length 50;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KAEYKKNKRRH 11  
Db 2 KAEYKKNKRRH 12  
1 KAEYKKNKRRH 12

RESULT 4  
US-09-180-422B-12  
Sequence 12; Application US/09180422B  
Patent No. 644644  
GENERAL INFORMATION:  
APPLICANT: BRUCKDORFER, KARL R  
TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED  
FROM APOLIPOPROTEIN B-100  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSER: NIXON & VANDERHAYE, P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/180,422B  
FILING DATE: 07-Dec-1998  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36663  
REFERENCE/DOCKET NUMBER: 117-268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164100  
TELEFAX: 7038164000  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 138 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-180-422B-12  
Query Match  
Best Local Similarity 95.2%; Score 60; DB 4; Length 138;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KAEYKKNKRRH 11  
Db 48 KAEYKKNKRRH 58  
1 KAEYKKNKRRH 58

RESULT 5  
US-09-079-030-83  
Sequence 83; Application US/09079030

Patent No. 6635623  
GENERAL INFORMATION:  
APPLICANT: Guevera, Jr., Juan G.  
APPLICANT: Hoogveen, Ron C.  
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY  
VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS  
NUMBER OF SEQUENCES: 229  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,030  
FILING DATE: Concurrently Herewith  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMillian, Nabeha R.  
REGISTRATION NUMBER: P-43,363  
REFERENCE/DOCKET NUMBER: ARAG:003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 83:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 394 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-09-079-030-83

Query Match 95.2% Score 60; DB 4; Length 394;  
Best Local Similarity 90.9% Pred. No. 0.013;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKNGRRH 11  
||:|||||  
Db 218 KAQYKNGRRH 228

RESULT 6  
US-09-079-030-214  
Sequence 214, Application US/09079030  
Patent No. 6635623  
GENERAL INFORMATION:  
APPLICANT: Guevera, Jr., Juan G.  
APPLICANT: Hoogveen, Ron C.  
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY  
VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS  
NUMBER OF SEQUENCES: 229  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,030

FILING DATE: Concurrently Herewith  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMillian, Nabeha R.  
REGISTRATION NUMBER: P-43,363  
REFERENCE/DOCKET NUMBER: ARAG:003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 214:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-09-079-030-214

Query Match 95.2% Score 60; DB 4; Length 840;  
Best Local Similarity 90.9% Pred. No. 0.028;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKNGRRH 11  
||:|||||  
Db 447 KAQYKNGRRH 457

RESULT 7  
US-09-180-422B-27  
Sequence 27, Application US/09180422B  
Patent No. 6444644  
GENERAL INFORMATION:  
APPLICANT: BRUCKDORFER, KARL R  
ETTELATE, CAMILLE  
TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED  
FROM APOLIPOPROTEIN B-100  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE, P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/180,422B  
FILING DATE: 07-Dec-1998  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36663  
REFERENCE/DOCKET NUMBER: 117-268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164100  
TELEFAX: 7038164100  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4536 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-180-422B-27

Query Match 95.2% Score 60; DB 4; Length 4536;  
Best Local Similarity 90.9% Pred. No. 0.15;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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us-10-657-404a-1.ral

OY 1 KAEYKXKRRH 11  
DB 3147 KAEYKXKRRH 3157

RESULT 8

US-09-079-030-1  
Sequence 1, Application US/09079030  
Patent No. 663623  
GENERAL INFORMATION:  
APPLICANT: Guevera, Jr., Juan G.  
APPLICANT: Hoogveen, Ron C.  
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY  
NUMBER OF SEQUENCES: 229  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 60/074,497  
FILING DATE: 30-APR-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Thomas  
REGISTRATION NUMBER: 29258  
REFERENCE/DOCKET NUMBER: 7991-015-999  
TELEPHONE: 215-504-4444  
TELEFAX: 215-504-4545  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4563 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-079-030-1  
TOPOLOGY: linear

Query Match  
Best Local Similarity 95.2%; Score 60; DB 4; Length 4536;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KAEYKXKRRH 11  
DB 3147 KAEYKXKRRH 3157

RESULT 9

US-09-108-006C-1  
Sequence 1, Application US/09108006C  
Patent No. 6524613  
GENERAL INFORMATION:  
APPLICANT: Steer, Clifford J.  
Kren, Betsy T.  
Bandyopadhyay, Parmita  
Roy-Chowdhury, Jayanta  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Kimeragen, Inc.  
STREET: 300 Pleasant Run  
CITY: Newtown  
STATE: PA  
COUNTRY: USA

ZIP: 18940

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: PaeSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/108.006C  
FILING DATE: 30-Jun-1992  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/054,288  
FILING DATE: 30-APR-1997  
APPLICATION NUMBER: 60/054,837  
FILING DATE: 05-AUG-1997  
APPLICATION NUMBER: 60/064,996  
FILING DATE: 10-NOV-1997  
APPLICATION NUMBER: 60/074,497  
FILING DATE: 12-FEB-1998  
APPLICATION NUMBER: PCT US 98/08834  
FILING DATE: 30-APR-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Thomas  
REGISTRATION NUMBER: 29258  
REFERENCE/DOCKET NUMBER: 7991-015-999  
TELEPHONE: 215-504-4444  
TELEFAX: 215-504-4545  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4563 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-108-006C-1

Query Match  
Best Local Similarity 95.2%; Score 60; DB 4; Length 4563;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KAEYKXKRRH 11  
DB 3174 KAEYKXKRRH 3184

RESULT 10

US-09-538-092-842  
Sequence 842, Application US/09538092  
Patent No. 6753314  
GENERAL INFORMATION:  
APPLICANT: Glot, Iolc  
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
FILE REFERENCE: 15966-542  
CURRENT APPLICATION NUMBER: US/09/538.092  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: 60/127,352  
PRIOR FILING DATE: 1999-04-01  
NUMBER OF SEQ ID NOS: 1587  
SOFTWARE: CuratSeqFormat Version 0.9  
SEQ ID NO 842  
LENGTH: 4563  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (0)..(0)  
OTHER INFORMATION: Polypeptide Accession Number P04114



Thu Jan 13 09:04:54 2005

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLIC: Patentin Release #1.0, Version #1.25  
APPLICATION NUMBER:  
FILING DATE: 07-Dec-1998  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER:  
TELECOMMUNICATION INFORMATION: 117-268  
TELEPHONE: 7038164000  
TELEFAX: 7038164100  
SEQUENCE FOR SEQ ID NO: 1:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /note= "Xaa represents Ser or Tyr"  
NAME/KEY: Modified-site  
LOCATION: 13  
OTHER INFORMATION: /note= "Xaa represents Ser or Tyr"  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-180-422B-1  
Query Match  
Best Local Similarity 82.5%; Score 52; DB 4; Length 14;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KAEYKKNKRRH 11  
DB 1 KQXKKNKRRH 11  
RESULT 14  
US-09-079-030-204  
Sequence 204 Application US/09079030  
GENERAL INFORMATION:  
APPLICANT: Guevera, Jr., Juan G.  
APPLICANT: Hoogewegen, Ron C.  
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY  
NUMBER OF SEQUENCES: 229  
CORRESPONDENCE ADDRESS: VECTORS FOR TRANSCRIPTION OF EUKARYOTIC CELLS  
ADDRESSER: Arnold  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLIC: Patentin Release #1.0, Version #1.25  
APPLICATION NUMBER:  
FILING DATE: US/09/079 030  
CLASSIFICATION: Concurrently Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: McWilliam, Nabesela R.  
REGISTRATION NUMBER: P-43,363  
TELECOMMUNICATION INFORMATION: ARAG-003

us-10-657-404a-1.ral

TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
SEQUENCE FOR SEQ ID NO: 204:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: linear  
US-09-079-030-204  
Query Match  
Best Local Similarity 90.0%; Score 52; DB 4; Length 18;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KAEYKKNKRRH 10  
DB 9 KQYKKNKRRH 18  
RESULT 15  
US-09-180-422B-18  
Sequence 18 Application US/09180422B  
GENERAL INFORMATION:  
APPLICANT: BRUCKNER, KARL R  
TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED  
NUMBER OF SEQUENCES: FROM APOLIPROTEIN B-100  
CORRESPONDENCE ADDRESS: 27  
ADDRESSER: NIXON & VANDERHAYE, P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLIC: Patentin Release #1.0, Version #1.25  
APPLICATION NUMBER:  
FILING DATE: 07-Dec-1998  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER:  
TELECOMMUNICATION INFORMATION: 117-268  
TELEPHONE: 7038164000  
TELEFAX: 7038164100  
SEQUENCE FOR SEQ ID NO: 18:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: linear  
US-09-180-422B-18  
Query Match  
Best Local Similarity 81.0%; Score 51; DB 4; Length 14;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KAEYKKNKRRH 11  
DB 1 KQSKKNKRRH 11  
Search Completed: January 12, 2005, 13 33 15  
Job time . 26 9032 secs





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OM protein - protein search, using ew model

Run on: January 12, 2005, 13:31:02 ; Search time 88.3548 Seconds  
(without alignments)  
44,980 Million cell updates/sec

Title: US-10-657-404A-1  
Perfect score: 63  
Sequence: 1 KAEYKKNKRRH 11

Scoring table:  
BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1608061 seqs, 361289386 residues  
Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/1/pubpaa/FCI_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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16:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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18:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
19:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
20:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	11	9	US-09-269-533A-1
2	63	100.0	11	17	US-10-657-404A-1
3	60	95.2	20	15	US-10-333-313-2
4	60	95.2	24	15	US-10-333-313-5
5	60	95.2	3000	16	US-10-741-601-431
6	60	95.2	4563	9	US-09-870-759-128
7	60	95.2	4563	10	US-09-802-640-32
8	60	95.2	4563	10	US-09-751-708A-128
9	60	95.2	4563	14	US-10-403-902A-32
10	60	95.2	4563	16	US-10-741-601-432
11	60	95.2	4563	16	US-10-741-601-433
12	60	95.2	4563	17	US-10-428-817A-124
13	47	74.6	20	14	US-10-115-072-14

14	47	74.6	20	17	US-10-679-032-52	Sequence 52, Appl
15	44	69.8	68	17	US-10-425-115-343636	Sequence 343636,
16	44	69.8	73	17	US-10-425-115-324738	Sequence 324738,
17	44	69.8	160	15	US-10-424-599-249584	Sequence 249584,
18	44	69.8	201	15	US-10-425-114-70425	Sequence 70425, A
19	44	69.8	205	17	US-10-425-115-357812	Sequence 357812,
20	44	69.8	216	15	US-10-425-114-68080	Sequence 68080, A
21	44	69.8	218	17	US-10-425-115-313121	Sequence 313121,
22	44	69.8	899	16	US-10-437-963-123131	Sequence 123131,
23	41	65.1	217	17	US-10-425-115-218015	Sequence 218015,
24	41	65.1	218	15	US-10-425-115-64096	Sequence 64096, A
25	41	65.1	266	16	US-10-437-963-203619	Sequence 203619,
26	40	63.5	75	15	US-10-424-599-266570	Sequence 266570,
27	40	63.5	100	17	US-10-425-115-200681	Sequence 200681,
28	40	63.5	769	15	US-10-342-844-90	Sequence 90, Appl
29	39	61.9	54	17	US-10-425-115-198721	Sequence 845, App
30	39	61.9	54	17	US-10-425-115-198721	Sequence 198721,
31	39	61.9	79	17	US-10-425-115-326337	Sequence 326337,
32	39	61.9	488	16	US-10-437-963-178827	Sequence 178827,
33	38	60.3	125	17	US-10-425-115-218016	Sequence 218016,
34	38	60.3	345	15	US-10-289-762-89	Sequence 89, Appl
35	38	60.3	487	15	US-10-282-122A-51517	Sequence 51517, A
36	37	58.7	68	10	US-09-764-891-4346	Sequence 4346, Ap
37	37	58.7	68	14	US-10-205-428-375	Sequence 375, App
38	37	58.7	79	15	US-10-424-599-245751	Sequence 245751,
39	37	58.7	84	14	US-10-023-896-61	Sequence 61, Appl
40	37	58.7	84	15	US-10-023-896-88	Sequence 88, Appl
41	37	58.7	86	15	US-10-424-599-234991	Sequence 234991,
42	37	58.7	88	17	US-10-425-115-360031	Sequence 360031,
43	37	58.7	89	14	US-10-029-186-29235	Sequence 29235, A
44	37	58.7	97	9	US-09-925-300-944	Sequence 944, App
45	37	58.7	127	17	US-10-425-115-191644	Sequence 191644,

ALIGNMENTS

*Application*

RESULT 1  
US-09-269-533A-1  
Sequence 1, Application US/09269533A  
Patent No. US20020147304A1  
GENERAL INFORMATION:  
APPLICANT: University of Strathclyde  
APPLICANT: Halbert, Gavin  
APPLICANT: Owens, Molira  
TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle  
FILE REFERENCE: P078985US  
CURRENT APPLICATION NUMBER: US/09/269, 533A  
CURRENT FILING DATE: 1999-06-01  
PRIOR APPLICATION NUMBER: PCT/GB97/02610  
PRIOR FILING DATE: 1997-09-25  
PRIOR APPLICATION NUMBER: GB 9620153.8  
PRIOR FILING DATE: 1996-09-27  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1..1)  
OTHER INFORMATION: Apo B binding site sequence  
US-09-269-533A-1

Query Match 100.0%; Score 63; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0015;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 KAEYKKNKRRH 11  
Db 1 KAEYKKNKRRH 11

RESULT 2  
US-10-657-404a-1  
Sequence 1, Application US/10657404A  
Publication No. US20040235730A1  
GENERAL INFORMATION:  
APPLICANT: University of Strathclyde  
APPLICANT: Halbert, Gavin  
APPLICANT: Owens, Molra  
TITLE OF INVENTION: Non-naturally Occurring Lipoprotein Particle  
FILE REFERENCE: P07885US-CIP  
CURRENT APPLICATION NUMBER: US/10/657,404A  
PRIOR FILING DATE: 2003-09-08  
PRIOR APPLICATION NUMBER: PCT/GB97/02610  
PRIOR FILING DATE: 1997-09-25  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Apo B binding site sequence  
US-10-657-404a-1

Query Match  
Best Local Similarity 100.0%; Score 63; DB 17; Length 11;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11  
DB 1 KAEYKKNKRRH 11

RESULT 3  
US-10-333-313-2  
Sequence 2, Application US/10333313  
Publication No. US20040091934A1  
GENERAL INFORMATION:  
APPLICANT: Narvonen, Outi  
TITLE OF INVENTION: Peptides and Their Use in Assays for Cardiovascular Disease  
FILE REFERENCE: GJE-6363  
CURRENT APPLICATION NUMBER: US/10/333,313  
PRIOR FILING DATE: 2003-01-15  
PRIOR APPLICATION NUMBER: PCT/GB01/03212  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: oligopeptide  
US-10-333-313-2

Query Match  
Best Local Similarity 95.2%; Score 60; DB 15; Length 20;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11  
DB 4 KAEYKKNKRRH 14

RESULT 4  
US-10-333-313-5

Sequence 5, Application US/10333313  
Publication No. US20040091934A1  
GENERAL INFORMATION:  
APPLICANT: Narvonen, Outi  
TITLE OF INVENTION: Peptides and Their Use in Assays for Cardiovascular Disease  
FILE REFERENCE: GJE-6363  
CURRENT APPLICATION NUMBER: US/10/333,313  
PRIOR FILING DATE: 2003-01-15  
PRIOR APPLICATION NUMBER: PCT/GB01/03212  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 24  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: oligopeptide  
US-10-333-313-5

Query Match  
Best Local Similarity 95.2%; Score 60; DB 15; Length 24;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11  
DB 6 KAEYKKNKRRH 16

RESULT 5  
US-10-741-601-431  
Sequence 431, Application US/10741601  
Publication No. US20040166519A1  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: GI001500  
CURRENT APPLICATION NUMBER: US/10/741,601  
PRIOR FILING DATE: 2003-12-22  
NUMBER OF SEQ ID NOS: 26415  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 431  
LENGTH: 3000  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-741-601-431

Query Match  
Best Local Similarity 95.2%; Score 60; DB 16; Length 3000;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11  
DB 2126 KAEYKKNKRRH 2136

RESULT 6  
US-09-870-759-128  
Sequence 128, Application US/09870759  
Patent No. US20020177551A1  
GENERAL INFORMATION:  
APPLICANT: TERMAN, David S  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
FILE REFERENCE: 870759  
CURRENT APPLICATION NUMBER: US/09/870,759  
PRIOR FILING DATE: 2002-01-14  
PRIOR APPLICATION NUMBER: US 60/208,128  
NUMBER OF SEQ ID NOS: 166  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 128

LENGTH: 4563  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-870-759-128

Query Match  
Best Local Similarity 95.2%; Score 60; DB 9; Length 4563;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11  
Db 3174 KAOYKKNKRRH 3184

RESULT 7  
US-09-802-640-32  
Sequence 32, Application US/09802640  
Publication No. US20030036057A1  
GENERAL INFORMATION:  
APPLICANT: Braun, Andreas  
APPLICANT: Kleya Patrick  
TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: 24736-2048  
CURRENT APPLICATION NUMBER: US/09/802,640  
CURRENT FILING DATE: 2001-03-09  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 32  
LENGTH: 4563  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-802-640-32

Query Match  
Best Local Similarity 95.2%; Score 60; DB 10; Length 4563;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11  
Db 3174 KAOYKKNKRRH 3184

RESULT 8  
US-09-751-708A-128  
Sequence 128, Application US/09751708A  
Publication No. US20030157113A1  
GENERAL INFORMATION:  
APPLICANT: Terman, David S  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
FILE REFERENCE: 751708  
CURRENT APPLICATION NUMBER: US/09/751,708A  
CURRENT FILING DATE: 2002-10-15  
PRIOR APPLICATION NUMBER: US 60/173,371  
PRIOR FILING DATE: 1999-12-28  
NUMBER OF SEQ ID NOS: 166  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 128  
LENGTH: 4563  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-751-708A-128

Query Match  
Best Local Similarity 95.2%; Score 60; DB 10; Length 4563;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11  
Db 3174 KAOYKKNKRRH 3184

RESULT 9  
US-10-403-902A-32  
Sequence 32, Application US/10403902A  
Publication No. US20030224418A1  
GENERAL INFORMATION:  
APPLICANT: Braun, Andreas  
APPLICANT: Kleya, Patrick  
TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: 24736-2048B  
CURRENT APPLICATION NUMBER: US/10/403,902A  
CURRENT FILING DATE: 2003-07-21  
PRIOR APPLICATION NUMBER: 09/802,640  
PRIOR FILING DATE: 2001-03-09  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 32  
LENGTH: 4563  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-403-902A-32

Query Match  
Best Local Similarity 95.2%; Score 60; DB 14; Length 4563;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11  
Db 3174 KAOYKKNKRRH 3184

RESULT 10  
US-10-741-601-432  
Sequence 432, Application US/10741601  
Publication No. US20040166519A1  
GENERAL INFORMATION:  
APPLICANT: Cargill, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: CLO01500  
CURRENT APPLICATION NUMBER: US/10/741,601  
CURRENT FILING DATE: 2003-12-22  
NUMBER OF SEQ ID NOS: 26415  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 432  
LENGTH: 4563  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-741-601-432

Query Match  
Best Local Similarity 95.2%; Score 60; DB 16; Length 4563;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11  
Db 3174 KAOYKKNKRRH 3184

RESULT 11  
US-10-741-601-433  
Sequence 433, Application US/10741601  
Publication No. US20040166519A1  
GENERAL INFORMATION:  
APPLICANT: Cargill, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: CLO01500  
CURRENT APPLICATION NUMBER: US/10/741,601  
CURRENT FILING DATE: 2003-12-22  
NUMBER OF SEQ ID NOS: 26415  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 433  
LENGTH: 4563  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-741-601-433

Query Match  
Best Local Similarity 95.2%; Score 60; DB 16; Length 4563;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KAEYKKNKH 11  
DB 3174 KAEYKKNKH 3184

RESULT 12  
US-10-428-817A-124  
Sequence 124, Application US/10428817A  
Publication No. US20040214783A1  
GENERAL INFORMATION:  
APPLICANT: TERMAN, David S  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
CURRENT APPLICATION NUMBER: US/10/428,817A  
PRIOR FILING DATE: 2003-05-05  
PRIOR APPLICATION NUMBER: US 60/378,988  
PRIOR FILING DATE: 2002-05-08  
PRIOR APPLICATION NUMBER: US 60/389,366  
PRIOR FILING DATE: 2002-06-15  
PRIOR APPLICATION NUMBER: US 60/406,697  
PRIOR FILING DATE: 2002-08-28  
PRIOR APPLICATION NUMBER: US 60/406,750  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: US 60/415,310  
PRIOR FILING DATE: 2002-10-01  
PRIOR APPLICATION NUMBER: US 60/415,400  
PRIOR FILING DATE: 2002-10-02  
PRIOR APPLICATION NUMBER: US 60/438,686  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 124  
LENGTH: 4563  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-428-817A-124

Query Match  
Best Local Similarity 95.2%; Score 60; DB 17; Length 4563;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KAEYKKNKH 11  
DB 3174 KAEYKKNKH 3184

RESULT 13  
US-10-115-072-14  
Sequence 14, Application US/10115072  
Publication No. US20030105003A1  
GENERAL INFORMATION:  
APPLICANT: NILSSON, JAN  
TITLE OF INVENTION: PEPTIDE-BASED IMMUNIZATION THERAPY FOR TREATMENT OF  
TITLE OF INVENTION: ATHEROSCLEROSIS AND DEVELOPMENT OF PEPTIDE-BASED ASSAY  
FILE REFERENCE: 03940 0057  
CURRENT APPLICATION NUMBER: US/10/115,072  
PRIOR FILING DATE: 2002-08-20  
PRIOR APPLICATION NUMBER: 60/281,410  
PRIOR FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: SE 0101232-7

PRIOR FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: SE 0103754-8  
PRIOR FILING DATE: 2001-09-11  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 14  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-115-072-14

Query Match  
Best Local Similarity 74.6%; Score 47; DB 14; Length 20;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKH 9  
DB 12 KAEYKKNKH 20

RESULT 14  
US-10-679-032-52  
Sequence 52, Application US/10679032  
Publication No. US20040202653A1  
GENERAL INFORMATION:  
APPLICANT: NILSSON, JAN  
APPLICANT: CARLSSON, ROLAND  
APPLICANT: BENGTSSON, JENNY  
APPLICANT: STRANDBERG, LEIF  
TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR  
FILE REFERENCE: 7303CIP  
CURRENT APPLICATION NUMBER: US/10/679,032  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 52  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-679-032-52

Query Match  
Best Local Similarity 74.6%; Score 47; DB 17; Length 20;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKH 9  
DB 12 KAEYKKNKH 20

RESULT 15  
US-10-425-115-343636  
Sequence 343636, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: LA ROSA, Thomas J.  
APPLICANT: KOVALIC, David K.  
APPLICANT: ZHOU, Yihua  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
FILE REFERENCE: 38-21 (53222) B  
CURRENT APPLICATION NUMBER: US/10/425,115  
PRIOR FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 343636

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; LENGTH: 68
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRR4577_76558C.1.pep
US-10-425-115-343636

```

```

Query Match      69.8%; Score 44; DB 17; Length 68;
Best Local Similarity 77.8%; Pred. No. 9.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      3 EYKKKGRH 11
        |:|:|:|
Db      1 EHKKKGRH 9

```

Search completed: January 12, 2005, 13:52:49  
Job time : 89.3548 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 12, 2005, 13:13:31 ; Search time 20.2258 Seconds  
(without alignments)  
52.328 Million cell updates/sec

Title: US-10-657-404a-1  
Perfect score: 63  
Sequence: 1 KAEYKKNKRR 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	95.2	4563	1	LPHUB
2	54	85.7	596	2	apoliipoprotein B-1
3	48	76.2	269	2	apoliipoprotein B-1
4	48	76.2	269	2	apoliipoprotein B-1
5	48	76.2	1778	2	apoliipoprotein B-1
6	48	76.2	2629	2	apoliipoprotein B-1
7	45	71.4	274	2	apoliipoprotein B-1
8	43	68.3	784	2	apoliipoprotein B-1
9	41.5	65.9	221	2	apoliipoprotein B-1
10	41.5	65.9	221	2	apoliipoprotein B-1
11	41.5	65.9	221	2	apoliipoprotein B-1
12	39	61.9	102	2	apoliipoprotein B-1
13	39	61.9	102	2	apoliipoprotein B-1
14	39	61.9	102	2	apoliipoprotein B-1
15	39	61.9	102	2	apoliipoprotein B-1
16	39	61.9	102	2	apoliipoprotein B-1
17	38	60.3	321	2	apoliipoprotein B-1
18	38	60.3	321	2	apoliipoprotein B-1
19	38	60.3	321	2	apoliipoprotein B-1
20	38	60.3	321	2	apoliipoprotein B-1
21	38	60.3	321	2	apoliipoprotein B-1
22	37	58.7	193	2	apoliipoprotein B-1
23	37	58.7	193	2	apoliipoprotein B-1
24	37	58.7	193	2	apoliipoprotein B-1
25	37	58.7	193	2	apoliipoprotein B-1
26	37	58.7	193	2	apoliipoprotein B-1
27	37	58.7	193	2	apoliipoprotein B-1
28	37	58.7	193	2	apoliipoprotein B-1
29	36	57.1	192	2	apoliipoprotein B-1

30	36	57.1	208	2	D65041
31	36	57.1	275	2	E60950
32	36	57.1	324	2	T24819
33	36	57.1	354	2	AD1038
34	36	57.1	370	2	T37282
35	36	57.1	416	2	D71936
36	36	57.1	416	2	G64647
37	36	57.1	565	2	T47423
38	36	57.1	611	2	E71318
39	36	57.1	800	2	T00034
40	36	57.1	1818	1	S73852
41	35	55.6	123	2	S61173
42	35	55.6	138	2	S06571
43	35	55.6	217	2	UC7997
44	35	55.6	224	2	S77828
45	35	55.6	227	2	B84667

## ALIGNMENTS

RESULT 1  
LPHUB  
N:Contains: apoliipoprotein B-26; apoliipoprotein B-48; apoliipoprotein B-74  
C:Species: Homo sapiens (man)  
C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 09-Jul-2004  
C:Accession: A27850; A25679; A25263; A25267; A25266; A24320; A24684; A23817; A25774; A264452; I61909; I59510; I39474; I39469; I84624; I37179; P50058  
R:Ludwig, E.H.; Blackhart, B.D.; Pierotti, V.R.; Catali, L.; Fortier, C.; Knott, T.; Sco  
DNA 6, 363-372, 1987  
A:Title: DNA sequence of the human apoliipoprotein B gene.  
A:Reference number: A27850; MUID:86003574; PMID:3652907  
A:Accession: A27850  
A:Molecule type: DNA  
A:Residues: 1-617, 'A', 619-1929, 'F', 1931-3318, 'D', 3320-3426, 'T', 3428-3431, 'Q', 3433-3731, 'A'  
A:Cross-references: UNIPROT:P04114; UNIPROT:P78482; UNIPROT:P78479; UNIPROT:Q9UMN0; UNIP  
R:Cladaras, C.; Hadzopoulos-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.  
EMBO J. 5, 3495-3507, 1986  
A:Title: The complete sequence and structural analysis of human apoliipoprotein B-100: re  
A:Reference number: A91058; MUID:87161758; PMID:3030729  
A:Accession: A25679  
A:Molecule type: mRNA  
A:Residues: 1-11, 15-2539, 'S', 2541-3823, 'R', 3825-4563 <CLA>  
A>Note: 1109-Aep was also found  
R:Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lusis, A.J.; Blackhart, B.; McCa  
Nucleic Acids Res. 14, 7501-7503, 1986  
A:Title: Complete cDNA and derived protein sequence of human apoliipoprotein B-100.  
A:Reference number: A93639; MUID:87016385; PMID:3763409  
A:Accession: A25263  
A:Molecule type: mRNA  
A:Residues: 1-272, 'N', 274-617, 'A', 619-1217, 'E', 1219-2091, 'V', 2093-2364, 'T', 2366-2679, 'Q'  
A:Cross-references: GB:X04506; NID:G34330; PIDN:CAA28191.1; PID:34331  
R:Law, S.W.; Grant, S.M.; Higuchi, K.; Hospattankar, A.; Lackner, K.; Lee, N.; Brewer Jr  
Proc. Natl. Acad. Sci. U.S.A. 83, 8143-8146, 1986  
A:Title: Human liver apoliipoprotein B-100 cDNA: complete nucleic acid and derived amino  
A:Reference number: A94134; MUID:87041416; PMID:3464946  
A:Accession: A25267  
A:Molecule type: mRNA  
A:Residues: 1-617, 'A', 619-703, 'P', 705-792, 'R', 794-1270, 'S', 1272-1866, 'G', 1868-2036, 'N', 2  
4189-4220, 'W', 4222-4563 <LAW>  
A>Note: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and  
R:Chen, S.H.; Yang, C.Y.; Chen, P.F.; Setzer, D.; Tanimura, M.; Li, W.H.; Goico Jr., A.M  
J. Biol. Chem. 261, 12918-12921, 1986  
A:Title: The complete cDNA and amino acid sequence of human apoliipoprotein B-100.  
A:Reference number: A92556; MUID:87008488; PMID:3759943  
A:Accession: A25266  
A:Molecule type: mRNA  
A:Residues: 1-97, 'T', 99-328, 'V', 330-644, 'I', 646-918, 'P', 920-3318, 'D', 3320-3426, 'T', 3428-  
9-4132, 'G', 4134-4180, 'E', 4182-4563 <CH>  
A:Cross-references: GB:U02610; NID:G178803; PIDN:AAA35549.1; PID:G178804  
A>Note: a total of 2366 residues were confirmed by direct sequencing of tryptic peptides  
R:Procter, A.A.; Hardman, D.A.; Sato, K.Y.; Schilling, J.W.; Yamana, M.; Hott, Y.J.; H

Proc. Natl. Acad. Sci. U.S.A. 83, 5678-5682, 1986  
 A>Title: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein B  
 A'Reference number: A24320; MUID:86287319; PMID:3461454  
 A'Accession: A24320  
 A'Molecule type: mRNA  
 A'Residuals: 1-97, 'I', 99-617, 'A', 619-941, 'YYIMSLPPKP', 951-1138, 'PTGRLPNCFNSNGILCYSLMHSFDF  
 A'Cross-references: GB:M14081; NID:9178795; PIDN:AAA51752.1; PID:9553189  
 R'LeW, S.W.; Lackner, K.J.; Hospattankar, A.V.; Anchors, J.M.; Sakaguchi, A.Y.; Naylor, A.  
 A'Title: Human apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of  
 A'Reference number: A24684; MUID:86094221; PMID:3001697  
 A'Accession: A24684  
 A'Molecule type: mRNA  
 A'Residuals: 485-617, 'A', 619-1044 <LA2>  
 A'Cross-references: GB:M12480; NID:9178791; PIDN:AAA51751.1; PID:9178792  
 R'Pictor, A.A.; Hardman, D.A.; Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; K  
 A'Title: Isolation of a cDNA clone encoding the amino-terminal region of human apolipop  
 A'Reference number: A94088; MUID:86149325; PMID:3513177  
 A'Accession: A23817  
 A'Molecule type: mRNA  
 A'Residuals: 1-291 <PRO>  
 A'Cross-references: GB:M12681; NID:9178797; PIDN:AAA51753.1; PID:9178798  
 R'Debb, S.S.; Motulsky, A.G.; Albers, J.J.  
 A'Title: A partial cDNA clone for human apolipoprotein B  
 A'Reference number: A25774; MUID:95270450; PMID:3860836  
 A'Accession: A25774  
 A'Molecule type: mRNA  
 A'Residuals: 709-791, 'SSSMKASHCPSHAGD', 810-906 <DEB>  
 A'Cross-references: GB:K03175; NID:9178821; PIDN:AAA51759.1; PID:9178822  
 R'Carlsson, P.; Darnfor, C.; Olofsson, S.O.; Bjurell, G.  
 A'Title: Analysis of the human apolipoprotein B gene: complete structure of the B-74 reg  
 A'Reference number: A91565; MUID:87191999; PMID:2883086  
 A'Accession: A26533  
 A'Molecule type: mRNA  
 A'Residuals: 1282-2721, 2742-3290, 'L', 3292-3336, 'N', 3338-3948, 'F', 3950-3963, 'Y', 3965-4180,  
 A'Cross-references: GB:M15421; NID:9178817; PIDN:AAA51758.1; PID:9178818  
 R'Hartman, D.A.; Procter, A.A.; Chen, G.C.; Schilling, J.W.; Sato, K.Y.; Lau, K.; Yamana  
 A'Title: Structural comparison of human apolipoproteins B-48 and B-100.  
 A'Reference number: A29671; MUID:88050832; PMID:3676265  
 A'Accession: A29671  
 A'Molecule type: mRNA  
 A'Residuals: 1671-2323, 'PYW', 2327-2352, 'H', 2354-2398 <HAR>  
 A'Cross-references: GB:M17367; NID:9178731; PIDN:AAA51741.1; PID:9178732  
 R'Shoulters, C.C.; Myant, N.B.; Sicoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E.;  
 A'Title: Molecular cloning of human LDL apolipoprotein B cDNA. Evidence for more than on  
 A'Reference number: A90084; MUID:86130855; PMID:3841481  
 A'Accession: A23287  
 A'Molecule type: mRNA  
 A'Residuals: 3846-4298 <SHO>  
 R'Piltzner, R.; Magener, R.; Stoffel, W.  
 A'Title: Isolation, expression and characterization of a human apolipoprotein B 100-spec  
 A'Reference number: A25572; MUID:87076044; PMID:3024665  
 A'Accession: A25572  
 A'Molecule type: mRNA  
 A'Residuals: 4219-4337, 'S', 4339-4563 <PFI>  
 A'Cross-references: GB:M36676  
 R'Mel, C.F.; Chen, S.H.; Yang, C.Y.; Marcel, Y.L.; Milne, R.W.; Li, W.H.; Sparrow, J.T.;  
 A'Title: Isolation, expression and characterization of a human apolipoprotein B 100-spec  
 A'Reference number: A24738; MUID:86042646; PMID:2932736  
 A'Accession: A24738  
 A'Molecule type: mRNA  
 A'Residuals: 'N', 3729-3731, 'I', 3733-3875, 'A', 3877-3948, 'F', 3950-3963, 'Y', 3965-3982, 'S', 39  
 A'Cross-references: GB:M12413; NID:9178735; PIDN:AAA51742.1; PID:9178736  
 R'Chen, S.H.; Habb, G.; Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silbermann, S.R.; Cai  
 A'Title: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in  
 A'Reference number: A40133; MUID:88018019; PMID:3659919

A'Accession: B40133  
 A'Molecule type: mRNA  
 A'Residuals: 2155-2179 <CH1>  
 A'Cross-references: GB:M18036; NID:9178799; PIDN:AAA51754.1; PID:9178800  
 A>Note: this mRNA includes the stop codon of the organ-specific mRNA for apo48  
 A'Accession: A40133  
 A'Molecule type: protein  
 A'Residuals: 51-75, 101-110, 128-139, 158-174, 197-207, 276-287, 298-304, 306-314, 526-532, 538-5  
 A>Note: These fragments were derived from apo48  
 R'Hartman, D.A.; Procter, A.A.; Schilling, J.W.; Kane, J.P.  
 A'Title: Carboxyl terminal analysis of human B-48 protein confirms the novel mechanism  
 A'Reference number: A28002; MUID:88106542; PMID:3426612  
 A'Accession: A28002  
 A'Molecule type: mRNA  
 A'Residuals: 2129-2179, 2181-2235 <HA2>  
 A'Cross-references: GB:M18471  
 A'Experimental source: Intestine  
 A>Note: This mRNA from intestine includes a stop codon created by RNA editing in place o  
 R'Mehrabian, M.; Schumaker, V.N.; Fares, G.C.; West, R.; Johnson, D.F.; Kirchgessner,  
 A'Title: Human apolipoprotein B: identification of cDNA clones and characterization of  
 A'Reference number: A24269; MUID:86041888; PMID:3903860  
 A'Accession: A24269  
 A'Molecule type: mRNA  
 A'Residuals: 3056-3159 <MRH>  
 A'Cross-references: GB:X03045; NID:928783; PIDN:CAA26850.1; PID:9292609  
 R'Hospattankar, A.V.; Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.B.  
 A'Title: Identification of a novel in-frame translational stop codon in human intestine  
 A'Reference number: A29659; MUID:88049670; PMID:2445342  
 A'Accession: A29659  
 A'Molecule type: mRNA  
 A'Residuals: 2169-2179 <HOS>  
 A>Note: The sequence shown represents the carboxyl end of apolipoprotein B-48  
 A'Accession: A29659; MUID:88049670; PMID:2445342  
 A'Molecule type: protein  
 A'Residuals: 28-41, 76-97, 'I', 99-100, 175-193, 206-215, 239-249, 259-266, 357-399, 455-490, 512-5  
 R'LeBoeuf, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Luisis, A.O.  
 A'Title: Human apolipoprotein B: partial amino acid sequence.  
 A'Reference number: A22006; MUID:84208786; PMID:6373369  
 A'Accession: A22006  
 A'Molecule type: protein  
 A'Residuals: 873-892, 'K', 894-896 <LE1>  
 A'Accession: B22006  
 A'Molecule type: protein  
 A'Residuals: 3113, 'L', 3115-3130, 'R', 3133-3133, 'P', 3135-3136, 'R', <LE2>  
 R'Blackhart, B.D.; Ludwig, E.M.; Pierotti, V.R.; Caiati, L.; Onasch, M.A.; Wallis, S.C.;  
 A'Title: Structure of the human apolipoprotein B gene.  
 A'Reference number: A92564; MUID:87057153; PMID:2946672  
 A'Accession: A92564  
 A'Molecule type: protein  
 A'Residuals: 419-425, 1987  
 R'Magener, R.; Piltzner, R.; Stoffel, W.  
 A'Title: Studies on the organization of the human apolipoprotein B 100 gene.  
 A'Reference number: A80715; MUID:87271140; PMID:2886136  
 A'Accession: A80715  
 A'Molecule type: protein  
 A'Residuals: 11097-11103, 1987  
 R'Wiesgraber, K.H.; Ball Jr., S.C.  
 A'Title: Human apolipoprotein B-100 heparin-binding sites.  
 A'Reference number: A92605; MUID:87280197; PMID:3301850  
 A'Accession: A92605  
 A'Molecule type: protein  
 A'Residuals: 28-41, 76-97, 'I', 99-100, 175-193, 206-215, 239-249, 259-266, 357-399, 455-490, 512-5

R:Daehli, N.; Lee, D.M.; Mok, T.  
Biochem. Biophys. Res. Commun. 137, 493-499, 1986  
A:Title: Apolipoprotein B is a calcium binding protein.  
A:Reference number: A90125; MUID:86242245; PMID:3087360  
A:Contents: annotation; calcium binding  
R:Carlsson, P.; Olofsson, S.O.; Bondjers, G.; Darnfors, C.; Wiklund, O.; Bjursell, G.  
Nucleic Acids Res. 13, 8813-8826, 1985  
A:Title: Molecular cloning of human apolipoprotein B cDNA.  
A:Reference number: 137178; MUID:86093680; PMID:3841204  
A:Accession: 137180

Query Match 95.2%; Score 60; DB 1; Length 4563;  
Best Local Similarity 90.9%; Pred. No. 0.063;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KAEYKKNKRRH 11  
||:|||||  
Db 3174 KAEYKKNKRRH 3184

## RESULT 2

apolipoprotein B - crab-eating macaque (fragment)  
C:Species: Macaca fascicularis (crab-eating macaque)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S32802  
R:Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchic  
Biochim. Biophys. Acta 1086, 326-334, 1991  
A:Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional re  
A:Reference number: S32802; MUID:92075708; PMID:1742325  
A:Accession: S32802  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-596 <PAP>  
A:Cross-references: UNIPROT:Q28473; EMBL:X15737; NID:G38047; PIDN:CAA33755.1; PID:G93012  
C:Superfamily: apolipoprotein B

Query Match 85.7%; Score 54; DB 2; Length 596;  
Best Local Similarity 81.8%; Pred. No. 0.1;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KAEYKKNKRRH 11  
||:|||||  
Db 15 KAEYKKNKRRH 25

## RESULT 3

apolipoprotein B-100 - golden hamster (fragment)  
C:Species: Mesocricetus auratus (golden hamster)  
C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C:Accession: C60950  
R:Law, A.; Scott, J.  
J. Lipid Res. 31, 1109-1120, 1990  
A:Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL  
A:Reference number: A60950; MUID:90324804; PMID:2373961  
A:Accession: C60950  
A:Molecule type: DNA  
A:Residues: 1-269 <LAW>  
A:Cross-references: UNIPROT:Q60537; UNIPROT:Q60536  
C:Superfamily: apolipoprotein B  
C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

Query Match 76.2%; Score 48; DB 2; Length 269;  
Best Local Similarity 72.7%; Pred. No. 0.56;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KAEYKKNKRRH 11  
||:|||||  
Db 9 KAEYKKNKRRH 19

## RESULT 4

## JH0102

apolipoprotein B - golden hamster (fragment)  
C:Species: Mesocricetus auratus (golden hamster)  
C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C:Accession: JH0102  
R:Smith, T.J.  
submitted to GenBank, June 1990  
A:Reference number: A38864  
A:Accession: JH0102  
A:Molecule type: DNA  
A:Residues: 1-779 <SMI>  
A:Cross-references: UNIPROT:Q60536; GB:M35187  
A:Note: this is a revision to the sequence from reference JH0101  
R:Smith, T.J.; Hautamaa, D.; Maeda, N.  
Gene 87, 309-310, 1990  
A:Title: Sequence of the putative low-density lipoprotein receptor-binding regions of ap  
A:Reference number: JH0101; MUID:90236327; PMID:2332175  
A:Contents: annotation  
A:Note: this sequence has been revised in reference A38864  
C:Genetics:  
A:Gene: apob  
C:Superfamily: apolipoprotein B  
C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;  
F:435-445/Region: receptor binding  
F:646-656/Region: receptor binding

Query Match 76.2%; Score 48; DB 2; Length 779;  
Best Local Similarity 72.7%; Pred. No. 1.5;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KAEYKKNKRRH 11  
||:|||||  
Db 435 KAEYKKNKRRH 445

## RESULT 5

apolipoprotein B - pig (fragments)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: J70382; I46567; I46568  
R:Maeda, N.; Ebert, D.L.; Doers, T.M.; Newman, M.; Hasler-Rapacz, J.; Attie, A.D.; Rapac  
Gene 70, 213-229, 1988  
A:Title: Molecular genetics of the apolipoprotein B gene in pigs in relation to atherosc  
A:Reference number: J70382; MUID:89108006; PMID:2905687  
A:Accession: J70382  
A:Molecule type: DNA  
A:Residues: 1-1778 <MAE>  
A:Cross-references: UNIPROT:Q29020; UNIPROT:Q29433  
R:Maeda, N.; Ebert, D.L.; Doers, T.M.; Newman, M.; Hasler-Rapacz, J.O.; Attie, A.D.; Rap

A:Title: Molecular genetics of the apolipoprotein B gene in pigs in relation to atherosc  
A:Reference number: I46567  
A:Accession: I46567  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-8, 'S', 10-238 <MA2>  
A:Cross-references: GB:M22646; NID:G164366; PIDN:AAA30996.1; PID:G164369  
A:Accession: I46568  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 239-1778 <MA3>  
A:Cross-references: GB:M22647; NID:G164367; PIDN:AAA30997.1; PID:G164370  
C:Comment: Apolipoprotein B is the predominant protein component of the low-density lipop

C:Superfamily: apolipoprotein B  
C:Keywords: atherosclerosis; cholesterol metabolism; LDL; lipid binding; lipoprotein

Query Match 76.2%; Score 48; DB 2; Length 1778;  
Best Local Similarity 72.7%; Pred. No. 3.3;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKKKRH 11  
Db 377 KAQYKKKKDKH 387

## RESULT 6

I46569  
apolipoprotein B - pig (fragment)  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004  
C/Accession: I46569  
R/Purell, C.; Maeda, N.; Ebert, D.L.; Kaiser, M.; Lund-Katz, S.; Sturley, S.L.; Kodoyia  
J. Lipid Res. 34, 1323-1335, 1993  
A/Title: Nucleotide sequence encoding the carboxyl-terminal half of apolipoprotein B  
A/Reference number: I46569; MUID:94014802; PMID:8409766  
A/Accession: I46569  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-2629 <PUB>  
A/Cross-references: UNIPROT:Q29021; GB:L11235; NID:g164371; PIDN:AAA74655.1; PID:g951375  
A/Genes: APOB  
A/Introns: 1984/1, 2022/2; 2083/3  
C/Superfamily: apolipoprotein B

Query Match  
Best Local Similarity 76.2%; Score 48; DB 2; Length 2629;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKKKRH 11  
Db 1227 KAQYKKKKDKH 1237

## RESULT 7

B60950  
apolipoprotein B-100 - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 31-Dec-1993 #sequence\_revision 09-Sep-1994 #text\_change 07-Oct-1994  
C/Accession: B60950  
R/Law, A.; Scott, J.  
J. Lipid Res. 31, 1109-1120, 1990  
A/Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL  
A/Reference number: A60950; MUID:90324804; PMID:2373961  
A/Accession: B60950  
A/Molecule type: mRNA  
A/Residues: 1-274 <LAW>  
A/Note: authors translated the codon ATA for residue 8 as Val  
C/Superfamily: apolipoprotein B  
C/Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

Query Match  
Best Local Similarity 71.4%; Score 45; DB 2; Length 274;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKKKRH 11  
Db 9 KAQYKKKKDKH 19

## RESULT 8

A60950  
apolipoprotein B-100 - rabbit (fragment)  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 31-Dec-1993 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
C/Accession: A60950  
R/Law, A.; Scott, J.  
J. Lipid Res. 31, 1109-1120, 1990  
A/Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL  
A/Reference number: A60950; MUID:90324804; PMID:2373961  
A/Accession: A60950

A/Molecule type: mRNA

A/Residues: 1-274 <LAW>

A/Cross-references: UNIPROT:Q7M29

A/Note: authors translated the codon GAT for residue 155 as His

C/Superfamily: apolipoprotein B

C/Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein.

## Query Match

Best Local Similarity 68.3%; Score 43; DB 2; Length 274;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 AEYKKKKRH 11  
Db 10 AKYKKKKRH 19

## RESULT 9

JH0101  
apolipoprotein B-100 - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C/Accession: JH0101; S33128; D60950  
R/Smith, T.V.; Hautamaa, D.; Maeda, N.  
Gene 87, 309-310, 1990  
A/Title: Sequence of the putative low-density lipoprotein receptor-binding regions of

A/Reference number: JH0101; MUID:90236327; PMID:2332175

A/Accession: JH0101

A/Molecule type: DNA

A/Residues: 1-784 <SMI>

A/Cross-references: UNIPROT:Q61314; GB:M35186

R/Smith, T.; Hautamaa, D.; Maeda, N.

Submitted to the EMBL Data Library, May 1989

A/Reference number: S33128

A/Accession: S33128

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-531, 'S', 533-784 <SM2>

R/Law, A.; Scott, J.

J. Lipid Res. 31, 1109-1120, 1990

A/Title: A cross-species comparison of the apolipoprotein B domain that binds to the L

A/Reference number: A60950; MUID:90324804; PMID:2373961

A/Accession: D60950

A/Molecule type: mRNA

A/Residues: 427-531, 'S', 533-700 <LAW>

C/Genetics:

A/Genes: MGI:Apob

A/Cross-references: MGI:88052

C/Superfamily: apolipoprotein B

C/Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein

F/46-656/Region: receptor binding

## Query Match

Best Local Similarity 68.3%; Score 43; DB 2; Length 784;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KAEYKKKKRH 11  
Db 435 KAQYKKKKDKH 445

## RESULT 10

E84675  
hypothetical protein At2g27670 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: E84675  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: AB4420; MUID:20083487; PMID:10617197  
A:Accession: B84675  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-221 <STO>  
A:Cross-references: UNIPROT:Q92UM9; GB:AE002093; NID:g3860265; PIDN:AACT3033.1; GSPDB:GN  
C:Gene: A12g27670  
A:Map position: 2

Query Match 65.9%; Score 41.5; DB 2; Length 221;  
Best Local Similarity 81.8%; Pred. No. 6.4;  
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Oy 1 KAEYKNGRHH 11  
|||  
58 KAEYKNG-HSH 67

Db 58 KAEYKNG-HSH 67

RESULT 11  
A54063  
TATA-binding protein-associated factor II - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 02-Aug-1994 #sequence\_revision 02-Aug-1994 #text\_change 09-Jul-2004  
C:Accession: A54063  
R:Vertlizer, C.P.; Yokomori, K.; Chen, J.L.; Tjian, R.  
Science 264, 933-941, 1994  
A:Title: Drosophila TAF-II 150: similarity to yeast gene TSM-1 and specific binding to C  
A:Reference number: A54063; MUID:94233377; PMID:8178153  
A:Accession: A54063  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-1213 <VER>  
A:Cross-references: UNIPROT:Q24325; GB:X79243; NID:G541664; PIDN:CAAS5830.1; PID:G541665  
C:Gene: FlyBase:Tafl150  
A:Cross-references: FlyBase:FBgn0011836

Query Match 65.1%; Score 41; DB 2; Length 1213;  
Best Local Similarity 63.6%; Pred. No. 39;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 KAEYKNGRHH 11  
|||  
Db 1154 KKEKKGRHKKH 1164

RESULT 12  
S09828  
hypotheetical protein UL65 - human cytomegalovirus (strain AD169)  
C:Species: human cytomegalovirus, human herpesvirus 5  
A>Note: host Homo sapiens (man)  
C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C:Accession: S09828  
R:Chen, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Hornsnel, T.;  
M.; Barrett, B.G.  
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990  
A:Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus  
A:Reference number: S09749; MUID:90269039; PMID:2161319  
A:Accession: S09828  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-102 <CHS>  
A:Cross-references: UNIPROT:P17148; EMBL:X17403; NID:G59591; PIDN:CAA35380.1; PID:G17808  
A>Note: this sequence was submitted to the EMBL Data Library, December 1989  
A>Note: this reading frame extends between two stop codons and does not begin with a start  
C:Superfamily: cyomegalovirus tegument protein

Query Match 61.9%; Score 39; DB 2; Length 102;  
Best Local Similarity 63.6%; Pred. No. 8.5;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 KAEYKNGRHH 11

Db 40 RAFAKTHRRH 50  
|||  
|||

RESULT 13  
T20958  
hypotheetical protein F15A4.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T20958  
R:Sim, M.  
submitted to the EMBL Data Library, October 1996  
A:Reference number: Z19350  
A:Accession: T20958  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-365 <WIL>  
A:Cross-references: UNIPROT:O17816; EMBL:Z81062; PIDN:CAB02945.2; GSPDB:GN00020; CESP:FL  
A:Experimental source: clone F15A4  
C:Gene: CESP:F15A4.1  
A:Map position: 2  
A:Introns: 96/1; 158/2; 210/3; 251/3; 296/2

Query Match 61.9%; Score 39; DB 2; Length 365;  
Best Local Similarity 70.0%; Pred. No. 28;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 AEYKNGRHH 11  
|||  
Db 214 AVMKNGRHH 223

RESULT 14  
H88337  
protein F15A4.1 (imported) - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: H88337  
R:anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog  
A:Reference number: A75000; MUID:99069613; PMID:9851916  
A>Note: see websites genome.wustl.edu/genC/elegans/ and www.sanger.ac.uk/Projects/C\_ele  
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A:Accession: H88337  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-452 <STO>  
A:Cross-references: UNIPROT:O17816; GB:chr\_II; PIDN:CAB02945.1; PID:G3875977; GSPDB:GN00  
C:Gene: F15A4.1  
A:Map position: 2

Query Match 61.9%; Score 39; DB 2; Length 452;  
Best Local Similarity 70.0%; Pred. No. 34;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 AEYKNGRHH 11  
|||  
Db 214 AVMKNGRHH 223

RESULT 15  
S44617  
C50C3.11 protein - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S44617  
R:Favell, A.D.  
submitted to the EMBL Data Library, May 1993  
A:Description: Sequence of the C. elegans coemid C50C3.  
A:Reference number: S44627

A:Accession: S44617  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-734 <FAV>  
 A:Cross-references: UNIPROT:P34374; EMBL:L14433; NID:g289649; PID:g289650  
 C:Genetics:  
 A:introns: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3

Query Match  
 Best Local Similarity 61.9%; Score 39; DB 2; Length 734;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAEYKKNR 10  
 :|||:||||  
 Db 65 RAELKSKNR 74

Search completed: January 12, 2005, 13:31:56  
 Job time : 21.2258 secs



RA Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,  
 RA Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.,  
 RA "Complete cDNA and derived protein sequence of human apolipoprotein B-  
 RT 100.";  
 RT Nucleic Acids Res. 14:7501-7503(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND VARIANT GLU-4181.  
 RX MEDLINE=88003974; PubMed=3652907;  
 RA Ludwig E.H., Blackhart B.D., Pierotti V.R., Caiati L., Fortier C.,  
 RA Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.,  
 RT "DNA sequence of the human apolipoprotein B gene.";  
 RT DNA 6:363-372(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.  
 RX MEDLINE=87008488; PubMed=3759943.  
 RA Chen S.-H., Yang C.-Y., Chan P.-F., Setzer D., Tanimura M., Li W.-H.,  
 RA Goto A.M., Jr., Chan L.,  
 RT "The complete cDNA and amino acid sequence of human apolipoprotein B-  
 RT 100.";  
 RT J. Biol. Chem. 261:12918-12921(1986).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87041416; PubMed=3464946;  
 RA Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,  
 RA Lee N., Brewer H.B., Jr.,  
 RT "Human liver apolipoprotein B-100 cDNA: complete nucleic acid and  
 RT derived amino acid sequence.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87161758; PubMed=3030729;  
 RA Cladatas C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.,  
 RA Zannis V.I.,  
 RT "The complete sequence and structural analysis of human apolipoprotein  
 RT B-100: relationship between apob-100 and apob-48 forms.";  
 RT EMBO J. 5:3495-3507(1986).  
 RN [6]  
 RP SEQUENCE OF 709-906 FROM N.A.  
 RX MEDLINE=85270450; PubMed=3860836;  
 RA Deeb S.S., Muculsky A.G., Albers J.J.,  
 RT "A partial cDNA clone for human apolipoprotein B.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985).  
 RN [7]  
 RP SEQUENCE OF 3056-3159 FROM N.A.  
 RX MEDLINE=86041888; PubMed=3903660;  
 RA Mehrlabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,  
 RA Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz B., Lusis A.J.,  
 RT "Human apolipoprotein B: identification of cDNA clones and  
 RT characterization of mRNA.";  
 RT Nucleic Acids Res. 13:6937-6953(1985).  
 RN [8]  
 RP SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A., AND VARIANT GLU-4181.  
 RX MEDLINE=86093680; PubMed=3841204;  
 RA Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O.,  
 RA Bjursell G.,  
 RT "Molecular cloning of human apolipoprotein B cDNA.";  
 RT Nucleic Acids Res. 13:8813-8826(1985).  
 RN [9]  
 RP SEQUENCE OF 3109-4563 FROM N.A.  
 RX MEDLINE=85300528; PubMed=2994225;  
 RA Knott T.J., Rall S.C., Jr., Innerarity T.L., Jacobson S.F., Urdan M.S.,  
 RA Levy-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M.,  
 RA Priestley L.M., Robertson E., Rall L.B., Betsholtz C., Shows T.B.,  
 RT "Human apolipoprotein B: structure of carboxyl-terminal domains, sites  
 RT of gene expression, and chromosomal localization.";  
 RT Science 230:37-43(1985).  
 RN [10]  
 RP SEQUENCE OF 1-291 FROM N.A.  
 RX MEDLINE=86149325; PubMed=3531177;  
 RA Procter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,  
 RA Chen G.C., Kirsher S.W., McIntire G., Kane J.P.,  
 RT "Isolation of a cDNA clone encoding the amino-terminal region of human  
 RT apolipoprotein B.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986).  
 RN [11]  
 RP SEQUENCE OF 1-1670 FROM N.A., AND VARIANT ILE-98.  
 RX MEDLINE=86287319; PubMed=3461454;  
 RA Procter A.A., Hardman D.A., Sato K.Y., Schilling J.W., Yamanaka M.,  
 RA Hott V.J., Herrild K.A., Chen G.C., Kane J.P.,  
 RT "Analysis of cDNA clones encoding the entire B-26 region of human  
 RT apolipoprotein B.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986).  
 RN [12]  
 RP PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-B48.  
 RX MEDLINE=88018019; PubMed=3659919;  
 RA Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,  
 RA Silbermann S.R., Gal S.-U., Deslypere J.P., Rosseneu M.,  
 RA Goto A.M., Jr., Li W.-H., Chan L.,  
 RT "Apolipoprotein B-48 is the product of a messenger RNA with an organ-  
 RT specific in-frame stop codon.";  
 RT Science 238:363-366(1987).  
 RN [13]  
 RP DOMAINS.  
 RX MEDLINE=87039351; PubMed=3773997;  
 RA Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C., Jr.,  
 RA Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,  
 RA Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,  
 RT "Complete protein sequence and identification of structural domains of  
 RT human apolipoprotein B.";  
 RT Nature 323:734-738(1986).  
 RN [14]  
 RP DOMAINS.  
 RA Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T.,  
 RA Tanimura M., Li W.-H., Sparrow D.A., DeLoof H., Rosseneu M.,  
 RA Lee F.-S., Gu Z.-W., Goto A.M., Jr., Chan L.,  
 RT "Sequence, structure, receptor-binding domains and internal repeats of  
 RT human apolipoprotein B-100.";  
 RT Nature 323:738-742(1986).  
 RN [15]  
 RP CALCULUM-BINDING DATA.  
 RX MEDLINE=86242245; PubMed=3087360;  
 RA Dashi N., Lee D.M., Mok T.,  
 RT "Apolipoprotein B is a calcium binding protein.";  
 RT Biochem. Biophys. Res. Commun. 137:493-499(1986).  
 RN [16]  
 RP PALMITOYLATION OF CY3-1112.  
 RX MEDLINE=20143590; PubMed=10679026;  
 RA Zhao Y., McCabe J.B., Vance J., Berthiaume L.G.,  
 RT "Palmitoylation of apolipoprotein B is required for proper  
 RT intracellular sorting and transport of cholesterol esters and  
 RT triglycerides.";  
 RT Mol. Biol. Cell 11:721-734(2000).  
 RN [17]  
 RP VARIANT SER-4338.  
 RX MEDLINE=91071750; PubMed=1979313;  
 RA Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P.,  
 RA Cuny G., Cambien F., Roizes G.,  
 RT "Detection by denaturing gradient gel electrophoresis of a new  
 RT polymorphism in the apolipoprotein B gene.";  
 RT Hum. Genet. 86:91-93(1990).  
 RN [18]  
 RP VARIANT FDB GLN-3527.  
 RX MEDLINE=89098975; PubMed=2563166;  
 RA Soris L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,  
 RA McCarthy B.J.,  
 RT "Association between a specific apolipoprotein B mutation and familial  
 RT defective apolipoprotein B-100.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).  
 RN [19]  
 RP VARIANT LEU-2739.  
 RX MEDLINE=91016974; PubMed=2216805;  
 RA Huang L.-S., Gavish D., Breslow J.L.,  
 RT "Sequence polymorphism in the human apob gene at position 8344.";  
 RT Nucleic Acids Res. 18:5922-5922(1990).

[20]  
 RN VARIANT FDB CYS-3558.  
 RP MEDLINE=95190020; PubMed=7883971;  
 RX Pullinger C.R., Hennessey L.K., Chatterton J.E., Liu W., Love J.A.,  
 RA Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.;  
 RT "Familial ligand-defective apolipoprotein B. Identification of a new  
 mutation that decreases LDL receptor binding affinity.";  
 RL J. Clin. Invest. 95:1225-1234(1995).  
 [21]  
 RN VARIANTS LEU-1437; SER-1914; LYS-2566; THR-3121; ALA-3945; MET-4128  
 RP AND THR-4481.  
 RX MEDLINE=97044521; PubMed=8889592;  
 RA Politzer O., Ricard S., Behague I., Souriau C., Evans A.E.,  
 RT Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;  
 RT "Detection of new variants in the apolipoprotein B (Apo B) gene by  
 PCR-SSCP.";  
 RL Hum. Mutat. 8:282-285(1996).  
 [22]  
 RN VARIANTS FDB GLN-3527 AND CYS-3558.  
 RX MEDLINE=97403938; PubMed=9259199;  
 RA Rabes J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G.,  
 RT Ktempf M., Giraudeau P., Junien C., Boileau C.;  
 RT "Familial ligand-defective apolipoprotein B-100: simultaneous  
 detection of the ARG3500-->GLN and ARG3511-->CYS mutations in a French  
 population.";  
 RL Hum. Mutat. 10:160-163(1997).  
 [23]  
 RN VARIANTS SER-1914; ARG-1923; LEU-2739; ASP-3319; THR-3427; GLN-3432  
 RP AND ILE-3921.  
 RX MEDLINE=98141125; PubMed=9490296;  
 RA Ieren T.P., Bakken K.S., Hoel V., Hjerremann I., Berg K.;  
 RT "Screening for mutations of the apolipoprotein B gene causing  
 RT hypochlolesterolemia.";  
 RL Hum. Genet. 102:44-49(1998).  
 CC -1- FUNCTION: Apolipoprotein B is a major protein constituent of  
 CC chylomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apo  
 CC B-100 functions as a recognition signal for the cellular binding  
 CC and internalization of LDL particles by the apoB/E receptor.  
 CC -1- SUBCELLULAR LOCATION: Secreted.

Query Match 95.2%; Score 60; DB 1; Length 4563;  
 Best Local Similarity 90.9%; Pred. No. 0.36;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAEYKXNKHRR 11  
 ||:|||||  
 DB 3174 KAOYKXNKHRR 3184

RESULT 3  
 ID 072600 PRELIMINARY; PRT; 4563 AA.  
 AC 072600;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Apolipoprotein B (Including Ag(X) antigen).  
 OS Name=APOB;  
 GN Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 CC NCBI\_TaxID=9606;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,  
 RA Ahearn M.O., Kuidanek S.A., Rajkumar N., Toch E.J., Yi O.,  
 RA Nickerson D.A.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY344608; AAP72970.1; -;  
 DR GO; GO:0005319; F:lipid transporter activity; IEA.  
 DR GO; GO:0006869; P:lipid transport; IEA.  
 DR InterPro; IPR009454; DUP1081.  
 DR InterPro; IPR001747; Lipid\_transport\_N.

DR Pfam; PF06448; DUP1081; 1.  
 DR Pfam; PF01347; Vitellinogen\_N; 1.  
 DR SMART; SM00638; LPD\_N; 1.  
 KW Lipoprotein.  
 SQ SEQUENCE 4563 AA; 515553 MW; 030B34167CEDC63C CRC64;

Query Match 95.2%; Score 60; DB 2; Length 4563;  
 Best Local Similarity 90.9%; Pred. No. 0.36;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAEYKXNKHRR 11  
 ||:|||||  
 DB 3174 KAOYKXNKHRR 3184

RESULT 4  
 ID 07YOR5 PRELIMINARY; PRT; 414 AA.  
 AC 07YOR5;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Apolipoprotein B 100 (Fragment).  
 GN Name=APOB-100;  
 OS Aotus vociferans (Spix's owl monkey).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.  
 CC NCBI\_TaxID=57176;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=22761261; PubMed=12878460;  
 RA Amling-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;  
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
 RT evidence for eutherian relationships.";  
 RL Mol. Phylogenet. Evol. 28:225-240(2003).  
 DR EMBL; AF548396; AAP97352.1; -;  
 KW Lipoprotein.  
 FT NON\_TER 1 1  
 FT NON\_TER 414 414  
 SQ SEQUENCE 414 AA; 45955 MW; EEPFA8492157E1BDE CRC64;

Query Match 90.5%; Score 57; DB 2; Length 414;  
 Best Local Similarity 81.8%; Pred. No. 0.095;  
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAEYKXNKHRR 11  
 ||:|||||  
 DB 47 KAOYKXNKHRR 57

RESULT 5  
 ID 028473 PRELIMINARY; PRT; 596 AA.  
 AC 028473;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Apolipoprotein B (Fragment).  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 CC Cercopithecinae; Macaca.  
 CC NCBI\_TaxID=9541;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Liver;  
 RC MEDLINE=92075708; PubMed=1742325;  
 RX Pape M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,  
 RA Marotti K.R., Welch G.W.;  
 RT "Apo B metabolism in the cynomolgus monkey: evidence for post-  
 RT transcriptional regulation.";  
 RL Biochim. Biophys. Acta 1086:336-334(1991).  
 RN [2]



DR EMBL; AF548425; AAP97381.1; -.  
KW Lipoprotein.  
FT NON\_TER 1  
SQ SEQUENCE 314 AA; 34719 MW; 3B5B34E780F0039E CRC64;  
Query Match 76.2%; Score 48; DB 2; Length 314;  
Best Local Similarity 72.7%; Pred. No. 2.9;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KAEYKKNKGRH 11  
||:|||||:  
Db 76 KAOYKKNKDKH 86  
RESULT 10  
Q7YOP3 PRELIMINARY; PRT; 316 AA.  
ID Q7YOP3  
AC Q7YOP3; 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Apolipoprotein B 100 (Fragment).  
GN Name=apob-100;  
OS Nandidia binctara (African palm civet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Viverridae; Nandiniinae;  
OC Nandidia.  
OX NCBI\_TaxID=71115;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22761261; PubMed=12878460;  
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;  
RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
evidence for eutherian relationships.";  
RL Mol. Phylogenet. Evol. 28:225-240(2003).  
DR EMBL; AF548420; AAP97376.1; -.  
KW Lipoprotein.  
FT NON\_TER 1  
SQ SEQUENCE 316 AA; 34540 MW; C04896B0E17562AE CRC64;  
Query Match 76.2%; Score 48; DB 2; Length 316;  
Best Local Similarity 72.7%; Pred. No. 2.9;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KAEYKKNKGRH 11  
||:|||||:  
Db 74 KAOYKKNKDKH 84  
RESULT 11  
Q7YON9 PRELIMINARY; PRT; 318 AA.  
ID Q7YON9  
AC Q7YON9; 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Apolipoprotein B 100 (Fragment).  
GN Name=apob-100;  
OS Zalophus californianus (California sealion).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Otariidae; Zalophus.  
OX NCBI\_TaxID=9704;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22761261; PubMed=12878460;  
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;  
RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
evidence for eutherian relationships.";  
RL Mol. Phylogenet. Evol. 28:225-240(2003).  
DR EMBL; AF548424; AAP97380.1; -.  
KW Lipoprotein.

FT NON\_TER 1  
SQ SEQUENCE 318 AA; 34888 MW; C04E7ECBA8B64C96 CRC64;  
Query Match 76.2%; Score 48; DB 2; Length 318;  
Best Local Similarity 72.7%; Pred. No. 2.9;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KAEYKKNKGRH 11  
||:|||||:  
Db 76 KAOYKKNKDKH 86  
RESULT 12  
Q7YOP7 PRELIMINARY; PRT; 411 AA.  
ID Q7YOP7  
AC Q7YOP7; 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Apolipoprotein B 100 (Fragment).  
GN Name=apob-100;  
OS Ochotona princeps (Southern American pika).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Ochotonidae; Ochotona.  
OX NCBI\_TaxID=9978;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22761261; PubMed=12878460;  
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;  
RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
evidence for eutherian relationships.";  
RL Mol. Phylogenet. Evol. 28:225-240(2003).  
DR EMBL; AF548414; AAP97370.1; -.  
KW Lipoprotein.  
FT NON\_TER 1  
SQ SEQUENCE 411 AA; 45696 MW; 077F419F951FF05A CRC64;  
Query Match 76.2%; Score 48; DB 2; Length 411;  
Best Local Similarity 72.7%; Pred. No. 3.8;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KAEYKKNKGRH 11  
||:|||||:  
Db 48 KAKYKKNKDKH 58  
RESULT 13  
Q7YOM8 PRELIMINARY; PRT; 436 AA.  
ID Q7YOM8  
AC Q7YOM8; 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Apolipoprotein B 100 (Fragment).  
GN Name=apob-100;  
OS Nyctimene albigenter (Common tube-nosed fruit bat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;  
OC Pteropodidae; Nyctimene.  
OX NCBI\_TaxID=48988;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22761261; PubMed=12878460;  
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;  
RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
evidence for eutherian relationships.";  
RL Mol. Phylogenet. Evol. 28:225-240(2003).  
DR EMBL; AF548435; AAP97391.1; -.  
KW Lipoprotein.  
FT NON\_TER 1  
SQ SEQUENCE 436 AA; 436 MW; 077F419F951FF05A CRC64;

SQ SEQUENCE 436 AA; 48717 MM; 1CA7EAD72D2C629 CRC64;  
 Query Match 76.2%; Score 48; DB 2; Length 436;  
 Best Local Similarity 72.7%; Pred. No. 4.1;  
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 KAEYKKNKRRH 11  
 ||:|||||:  
 Db 76 KAQYKKNKDKH 86

Query Match 76.2%; Score 48; DB 2; Length 436;  
 Best Local Similarity 72.7%; Pred. No. 4.1;  
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 KAEYKKNKRRH 11  
 ||:|||||:  
 Db 76 KAQYKKNKDKH 86

Search completed: January 12, 2005, 13:30:53  
 Job time : 110.645 secs

RESULT 14  
 Q7YOR4  
 ID Q7YOR4 PRELIMINARY; PRT; 438 AA.  
 AC Q7YOR4;  
 DT 01-OCT-2003 (TREMBlrel. 25, Created)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
 DE Apolipoprotein B 100 (Fragment).  
 GN Name=apOB-100;  
 OS Balaena mysticetus (Bowhead whale).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti; Balenidae;  
 OC Balaena.  
 OX NCBI\_TaxID=27602;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=22761261; PubMed=12878460;  
 RA Amrine-Madsen H.; Koepfli K.-P.; Wayne R.K.; Springer M.S.;  
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
 RL evidence for eutherian relationships."  
 RL Mol. Phylogenet. Evol. 28:225-240(2003).  
 DR EMBL; AF548397; AAP97353.1; -.  
 KW Lipoprotein.  
 FT NON\_TER 1  
 FT NON\_TER 438  
 SQ SEQUENCE 438 AA; 48849 MM; 48984F295035ADD0 CRC64;

Query Match 76.2%; Score 48; DB 2; Length 438;  
 Best Local Similarity 72.7%; Pred. No. 4.1;  
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11  
 ||:|||||:  
 Db 71 KAQYKKNKDKH 81

RESULT 15  
 Q7YR04  
 ID Q7YR04 PRELIMINARY; PRT; 438 AA.  
 AC Q7YR04;  
 DT 01-OCT-2003 (TREMBlrel. 25, Created)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
 DE Apolipoprotein B (Fragment).  
 OS Roussetus amplexicaudatus (Common roussette).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;  
 OC Pteropodinae; Roussetus.  
 OX NCBI\_TaxID=58083;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22761261; PubMed=12878460;  
 RA Amrine-Madsen H.; Koepfli K.-P.; Wayne R.K.; Springer M.S.;  
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
 RL evidence for eutherian relationships."  
 RL Mol. Phylogenet. Evol. 28:225-240(2003).  
 DR EMBL; AY243383; AAP50771.1; -.  
 KW Lipoprotein.  
 FT NON\_TER 1  
 FT NON\_TER 438  
 SQ SEQUENCE 438 AA; 48597 MM; 41C890DEAF95C872 CRC64;

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OM protein - protein search, using sw model

Run on: January 12, 2005, 12:47:25 ; Search time 101.484 Seconds  
(without alignments)  
38.883 Million cell updates/sec

Title: US-10-657-404A-2  
Perfect score: 54  
Sequence: 1 TTRLTRKRGK 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues  
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	54	100.0	11 2 AAW57205	AAW57205 Apo B bin
2	54	100.0	13 2 AAW57207	AAW57207 Apo B 100
3	54	100.0	15 2 AAW56892	AAW56892 ApoB-100
4	54	100.0	20 6 AB037575	AB037575 Heparin b
5	54	100.0	22 2 AAW57208	AAW57208 Apo B 100
6	54	100.0	22 2 AAW57209	AAW57209 Apo B 100
7	54	100.0	34 5 AAE14541	AAE14541 Human apo
8	54	100.0	36 2 AAW56876	AAW56876 Nucleic a
9	54	100.0	37 2 AAW64587	AAW64587 Human apo
10	54	100.0	51 2 AAW96845	AAW96845 Nucleic a
11	54	100.0	343 4 ABB37687	ABB37687 Peptide #
12	54	100.0	343 4 AAG52504	AAG52504 Human liv
13	54	100.0	377 2 AAR72704	AAR72704 Human apo
14	54	100.0	377 2 AAR34031	AAR34031 Sequence
15	54	100.0	2463 8 AD037400	AD037400 Human apo
16	54	100.0	3923 2 AAY31337	AAY31337 Human apo
17	54	100.0	4536 2 AAW41262	AAW41262 Apolipop
18	54	100.0	4536 2 AAW96826	AAW96826 Amino aci
19	54	100.0	4560 7 AAU98981	AAU98981 Human apo
20	54	100.0	4561 7 ADD48677	ADD48677 Human pro
21	54	100.0	4563 5 AAO15893	AAO15893 Human apo
22	54	100.0	4563 6 ABR40253	ABR40253 Human a1
23	54	100.0	4563 6 ABU79140	ABU79140 Apolipop
24	54	100.0	4563 7 ADF43408	ADF43408 Apolipop
25	54	100.0	4563 8 ADH18871	ADH18871 Human apo

26	54	100.0	4563 8 ADH18870	ADH18870 Human apo
27	54	100.0	4563 8 AD033445	AD033445 Human apo
28	54	100.0	4563 8 AD033447	AD033447 Human apo
29	54	100.0	4590 4 AAU33184	AAU33184 Novel hum
30	49	90.7	15 2 AAW41261	AAW41261 Apolipop
31	45	83.3	10 2 AAY30682	AAY30682 Apo-B100
32	45	83.3	10 2 AAY30687	AAY30687 Apo-B100
33	45	83.3	10 4 AAG94401	AAG94401 Human com
34	45	83.3	10 4 AAG94535	AAG94535 Human com
35	45	83.3	10 4 AAG94441	AAG94441 Human com
36	44	81.5	10 2 AAY30690	AAY30690 Apo-B100
37	44	81.5	10 2 AAY30692	AAY30692 Apo-B100
38	44	81.5	10 2 AAY30686	AAY30686 Apo-B100
39	44	81.5	10 2 AAY30688	AAY30688 Apo-B100
40	44	81.5	11 2 AAW57206	AAW57206 Apo B 100
41	44	81.5	11 2 AAW87717	AAW87717 Analogue
42	44	81.5	11 5 AAE21732	AAE21732 BSMR effe
43	44	81.5	11 6 ABU07938	ABU07938 Apoprotei
44	44	81.5	11 7 ADF56451	ADF56451 Human apo
45	44	81.5	12 2 AAW41260	AAW41260 Apolipop

## ALIGNMENTS

RESULT 1  
AAW57205  
ID AAW57205 standard; peptide; 11 AA.  
XX  
AC AAW57205;  
XX  
DT 03-AUG-1998 (first entry)  
XX  
DE Apo B binding site peptide 2.  
XX  
KW Apo B; binding site; receptor; cancer; drug delivery; anticancer;  
KW growth supplement; non-natural lipid particle; low density lipoprotein;  
KW LDL; receptor component; apo B100 receptor site.  
XX  
OS Synthetic.  
OS  
PN WO9813385-A2.  
XX  
PD 02-APR-1998.  
XX  
PP 25-SEP-1997; 97WO-GB002610.  
XX  
PR 27-SEP-1996; 96GB-00020153.  
XX  
PA (UYST ) UNIV STRATHCLYDE.  
XX  
PI Halbert GW, Owens MD, Baillie G;  
XX  
DR WPI, 1998-230637/20.  
XX  
PT Non-natural lipid particle comprising peptide binding to apo B protein  
PT receptor - useful as, e.g. vector for delivering drugs to cancer cells  
PT that express this receptor.  
XX  
PS Claim 12; Page 52; 73pp; English.  
XX  
CC The present sequence represents a specifically claimed Apo B binding site  
CC peptide which can be used as a component of a non-naturally occurring,  
CC receptor-competent low density lipoprotein (LDL) particle of the present  
CC invention. The LDL particle comprises at least 1 peptide component that  
CC has at least 1 binding site for an apo B protein receptor and at least 1  
CC lipophilic substituent. Also described in the invention are peptides  
CC containing an apo B binding sequence with at least 70% identity with  
CC sequences: KAEYKKNKRR (1) or TTRLTRKRGK (2), or their dimers. Non-  
CC naturally occurring, receptor-competent LDL particles are useful as: (i)  
CC drug-targeting vectors for delivering anticancer drugs to cancer cells  
CC that express an apo B protein receptor, and (ii) additives for cell  
CC culture media especially as growth supplements. Non-naturally occurring,

CC receptor-competent LDL particles do not require the complete apo B  
 CC sequence, which is large and tends to aggregate, to provide binding  
 CC affinity to an apo B protein receptor  
 XX  
 SQ Sequence 11 AA;

Query Match  
 Best Local Similarity 100.0%; Score 54; DB 2; Length 11;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 TTRLTRKRGK 11  
 1 TTRLTRKRGK 11

RESULT 2  
 AAW57207  
 ID AAW57207 standard; peptide; 13 AA.  
 AC  
 XX  
 XX AAW57207;  
 DT 03-AUG-1998 (first entry)  
 DE Apo B 100 binding site peptide analogue peptide B.  
 XX Apo B; binding site; receptor; cancer; drug delivery; anticancer;  
 KW growth supplement; non-natural lipid particle; low density lipoprotein;  
 KM LDL; receptor component; apo B100 receptor site.  
 XX  
 OS Synthetic.

FT Key Location/Qualifiers  
 Modified-site 1 /note= "attached to retinoic acid"  
 FT  
 XX WO9813385-A2.  
 XX 02-APR-1998.  
 XX  
 XX 25-SEP-1997; 97WO-GB002610.  
 XX PR 27-SEP-1996; 96GB-00020153.  
 XX PA (UYST) UNIV STRATHCLYDE.  
 XX PI Halbert GW, Owens MD, Baillie G;  
 XX WPI; 1998-230637/20.  
 XX

DR Non-natural lipid particle comprising peptide binding to apo B protein  
 XX receptor - useful as, e.g. vector for delivering drugs to cancer cells  
 XX that express this receptor.  
 PS Claim 13; Fig 7; 73pp; English.

CC The present sequence represents a specifically claimed Apo B 100 binding  
 CC site peptide analogue which can be used as a component of a non-  
 CC naturally occurring, receptor-competent low density lipoprotein (LDL)  
 CC peptide component that has at least 1 binding site for an apo B protein  
 CC receptor and at least 1 lipophilic substituent. Also described in the  
 CC invention are peptides containing an apo B binding sequence with at least  
 CC 70% identity with sequences: KAEYKNKRRH (1) or TTRLTRKRGK (2), or their  
 CC dimers. Non-naturally occurring, receptor-competent LDL particles are  
 CC useful as: (i) drug-targeting vectors for delivering anticancer drugs to  
 CC cancer cells that express an apo B protein receptor, and (ii) additives  
 CC for cell culture media especially as growth supplements. Non-naturally  
 CC occurring, receptor-competent LDL particles do not require the complete  
 CC apo B sequence, which is large and tends to aggregate, to provide binding  
 CC affinity to an apo B protein receptor  
 XX  
 SQ Sequence 13 AA;

Query Match  
 Best Local Similarity 100.0%; Score 54; DB 2; Length 13;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TTRLTRKRGK 11  
 2 TTRLTRKRGK 12

RESULT 3  
 AAW6892  
 ID AAW6892 standard; peptide; 15 AA.  
 AC  
 XX  
 XX AAW6892;  
 DT 22-APR-1999 (first entry)  
 DE Apob-100 nuclear localisation signal sequence, residues 3353-3367.  
 XX Human apolipoprotein B-100, apob-100; very-low density lipoprotein; VLDL;  
 KW apolipoprotein; binding; in vivo transport; nucleic acid; binding domain;  
 KM nuclear localisation sequence; gene therapy; cancer; cystic fibrosis;  
 XX non-small cell lung carcinoma; diabetes; arteriosclerosis.  
 OS Homo sapiens.

XX WO9856938-A1.  
 XX 17-DEC-1998.  
 XX  
 XX 10-JUN-1998; 98WO-US011927.  
 XX PF 13-JUN-1997; 97US-00874807.  
 XX PR 14-MAY-1998; 98US-00079030.  
 XX PA (BAYU) BAYLOR COLLEGE MEDICINE.  
 XX PI Guevara JG, Hoogvee RC, Moore JP;  
 XX WPI; 1999-070331/06.  
 XX

DR Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -  
 XX used for delivering nucleic acid to cells for gene therapy and antisense  
 XX treatment.  
 PS Claim 19; Fig 13D; 293pp; English.

CC AAW6892-97 represent nuclear localisation signal sequence derived from  
 CC human apolipoprotein B-100 (apob-100). Apob-100 is a major apoprotein  
 CC component of very-low density lipoproteins (VLDL), intermediate density  
 CC lipoprotein (IDL), low density lipoproteins (LDL) and lipoprotein a. The  
 CC present sequence can be used in the composition of the invention. The  
 CC specification describes a composition that comprises LDL and  
 CC apolipoproteins for the binding and in vivo transport of nucleic acids.  
 CC The composition is used to deliver nucleic acids to eukaryotic cells, in  
 CC vivo or in vitro, for expressing a therapeutic polypeptide or antisense  
 CC molecule (or ribozyme). Specifically they are used for gene therapy of  
 CC cancers (particularly non-small cell lung carcinoma), diabetes, cystic  
 CC fibrosis and arteriosclerosis  
 XX  
 SQ Sequence 15 AA;

Query Match  
 Best Local Similarity 100.0%; Score 54; DB 2; Length 15;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TTRLTRKRGK 11  
 5 TTRLTRKRGK 15

RESULT 4  
 ABJ37575

ID ABJ37575 standard; peptide; 20 AA.  
 XX  
 AC ABJ37575;  
 XX  
 DT 10-MAY-2003 (first entry)  
 XX  
 DE Heparin binding peptide sequence #28.  
 XX  
 KW Cytostatic; antineumatic; antiarthritic; antidiabetic; ophthalmological;  
 KW cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour;  
 KW rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003007689-A2.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 22-JUL-2002; 2002MO-US023419.  
 XX  
 PR 20-JUL-2001; 2001US-0306726P.  
 XX  
 PA (ETHZ-) ETH ZUERICH.  
 PA (UZYU-) UNIV ZURICH.  
 XX  
 PI Hubbell JA, Schoenmakers R, Maynard HD;  
 XX  
 DR WPI; 2003-300420/29.  
 XX  
 PT Use of a ligand comprising of at least one sulfated or sulfonated amino  
 PT acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic  
 PT retinopathy and hypoxia.  
 XX  
 PS Disclosure: Fig 2; 79pp; English.  
 XX  
 CC The invention relates to a novel ligand for binding a target biomolecule,  
 CC which comprises a peptide having at least one sulphated or sulphonated,  
 CC amino acid and at least one amino acid chosen from neutral and positively  
 CC charged amino acids. The novel ligands can be used for the treatment of  
 CC e.g. tumours, rheumatoid arthritis, diabetic retinopathy and hypoxia.  
 CC This sequence represents a heparin binding peptide relating to the  
 CC invention  
 CC  
 XX  
 SQ Sequence 20 AA;  
 XX  
 QY Query Match 100.0%; Score 54; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.004;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 TTRLTRKRGK 11  
 6 TTRLTRKRGK 16  
 DB

RESULT 5  
 AAM57208  
 ID AAM57208 standard; peptide; 22 AA.  
 XX  
 AC AAM57208;  
 XX  
 DT 03-AUG-1998 (first entry)  
 XX  
 DE Apo B 100 binding site peptide analogue peptide C.  
 XX  
 KW Apo B; binding site; receptor; cancer; drug delivery; anticancer;  
 KW growth supplement; non-natural lipid particle; low density lipoprotein;  
 KW LDL; receptor component; apo B100 receptor site.  
 XX  
 OS Synthetic.  
 XX  
 PN Key Location/Qualifiers  
 FT Modified-site 1 /note= "attached to retinoic acid"  
 FT

FT Modified-site 22  
 FT /note= "attached to cholesterol"  
 XX  
 PN WO9813385-A2.  
 XX  
 PD 02-APR-1998.  
 XX  
 PF 25-SEP-1997; 97WO-GB002610.  
 XX  
 PR 27-SEP-1996; 96GB-00020153.  
 XX  
 PA (UYST ) UNIV STRATHCLYDE.  
 XX  
 PI Halbert GW, Owens MD, Baillie G;  
 XX  
 DR WPI; 1998-230637/20.  
 XX  
 PT Non-natural lipid particle comprising peptide binding to apo B protein  
 PT receptor - useful as, e.g. vector for delivering drugs to cancer cells  
 PT that express this receptor.  
 XX  
 PS Claim 13; Fig 7; 73pp; English.  
 XX  
 CC The present sequence represents a specifically claimed Apo B 100 binding  
 CC site peptide analogue which can be used as a component of a non-  
 CC naturally occurring, receptor-competent low density lipoprotein (LDL)  
 CC particle of the present invention. The LDL particle comprises at least 1  
 CC peptide component that has at least 1 binding site for an apo B protein  
 CC receptor and at least 1 lipophilic substituent. Also described in the  
 CC invention are peptides containing an apo B binding sequence with at least  
 CC 70% identity with sequences: KAEYKNGHRH (1) or TTRLTRKRGK (2), or their  
 CC dimers. Non-naturally occurring, receptor-competent LDL particles are  
 CC useful as: (i) drug-targeting vectors for delivering anticancer drugs to  
 CC cancer cells that express an apo B protein receptor, and (ii) additives  
 CC for cell culture media especially as growth supplements. Non-naturally  
 CC occurring, receptor-competent LDL particles do not require the complete  
 CC apo B sequence, which is large and tends to aggregate, to provide binding  
 CC affinity to an apo B protein receptor  
 CC  
 XX  
 SQ Sequence 22 AA;  
 XX  
 QY Query Match 100.0%; Score 54; DB 2; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.0044;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 TTRLTRKRGK 11  
 6 TTRLTRKRGK 16  
 DB

RESULT 6  
 AAM57209  
 ID AAM57209 standard; peptide; 22 AA.  
 XX  
 AC AAM57209;  
 XX  
 DT 03-AUG-1998 (first entry)  
 XX  
 DE Apo B 100 binding site peptide analogue peptide D.  
 XX  
 KW Apo B; binding site; receptor; cancer; drug delivery; anticancer;  
 KW growth supplement; non-natural lipid particle; low density lipoprotein;  
 KW LDL; receptor component; apo B100 receptor site.  
 XX  
 OS Synthetic.  
 XX  
 PN Key Location/Qualifiers  
 FT Modified-site 1 /note= "attached to retinoic acid"  
 FT  
 XX  
 PN WO9813385-A2.  
 XX  
 PD 02-APR-1998.  
 XX

XX 25-SEP-1997; 97WO-GB002610.  
 PF 27-SEP-1996; 96GB-00020153.  
 XX (UYST ) UNIV STRATHCLYDE.  
 PA Halbert GW, Owens MD, Baillie G,  
 PI WPI; 1998-230637/20.  
 XX Non-natural lipid particle comprising peptide binding to apo B protein  
 PT receptor - useful as, e.g. vector for delivering drugs to cancer cells  
 XX that express this receptor.  
 PS Claim 13; Fig 7; 73pp; English.  
 CC The present sequence represents a specifically claimed Apo B 100 binding  
 CC site peptide analogue which can be used as a component of a non-  
 CC naturally occurring, receptor-competent low density lipoprotein (LDL)  
 CC particle of the present invention. The LDL particle comprises at least 1  
 CC peptide component that has at least 1 binding site for an apo B protein  
 CC receptor and at least 1 lipophilic substituent. Also described in the  
 CC invention are peptides containing an apo B binding sequence with at least  
 CC 70% identity with sequences: KAEYKMKRKH (1) or TTRLTRKRGK (2) or their  
 CC dimers. Non-naturally occurring, receptor-competent LDL particles are  
 CC useful as: (i) drug-targeting vectors for delivering anticancer drugs to  
 CC cancer cells that express an apo B protein receptor, and (ii) additives  
 CC for cell culture media especially as growth supplements. Non-naturally  
 CC occurring, receptor-competent LDL particles do not require the complete  
 CC apo B sequence, which is large and tends to aggregate, to provide binding  
 CC affinity to an apo B protein receptor  
 XX Sequence 22 AA;  
 SQ  
 Query Match Best Local Similarity 100.0%; Score 54; DB 2; Length 22;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTRLTRKRGK 11  
 DB 6 TTRLTRKRGK 16

DR WPI; 2002-179777/23.  
 XX New peptide useful in enzyme immunoassays for detecting oxidized low  
 PT density lipoprotein which is a marker of coronary heart disease and other  
 PT cardiovascular diseases, has affinity for oxidized low density  
 XX lipoprotein.  
 XX Claim 6; Page 5; 21pp; English.  
 CC The invention relates to peptides having affinity for oxidised low  
 CC density lipoprotein (oxLDL), in cyclised or multimeric form. The peptide  
 CC is useful in an immunoassay to determine the presence, and optionally,  
 CC the amount of antibodies in a sample, having affinity for oxLDL.  
 CC Preferably immobilised peptide is useful for measuring the amount of  
 CC autoantibodies for oxLDL in a sample, especially a serum or plasma sample  
 CC from a patient for evaluating the risk of coronary heart diseases, other  
 CC cardiovascular diseases, and several other disorders such as  
 CC periorbitis, pre-eclampsia, non-insulin-dependent diabetes and  
 CC endothelial dysfunction. The peptide of the invention is stable, can be  
 CC synthesised easily without the need to isolate proteins from a patient's  
 CC blood, and has a long half-life. The present sequence is human apob-100  
 XX derived peptide p62 used in the invention  
 SQ Sequence 34 AA;  
 Query Match Best Local Similarity 100.0%; Score 54; DB 5; Length 34;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTRLTRKRGK 11  
 DB 24 TTRLTRKRGK 34

RESULT 8  
 ID AAM96876  
 XX AAM96876 standard; peptide; 36 AA.  
 AC AAM96876;  
 XX  
 DT 22-APR-1999 (first entry)  
 XX  
 DE Nucleic acid binding domain from apob-100, residues 3348-3390.  
 XX  
 KW Human apolipoprotein B-100; apob-100; very-low density lipoprotein; VLDL;  
 KW apolipoprotein; binding; in vivo transport; nucleic acid; binding domain;  
 KW nuclear localisation sequence; gene therapy; cancer; cystic fibrosis;  
 XX non-small cell lung carcinoma; diabetes; arteriosclerosis.  
 OS Homo sapiens.  
 XX  
 DE Homo sapiens.  
 XX  
 EN WO9856938-A1.  
 XX  
 PD 17-DEC-1998.  
 XX  
 PF 10-JUN-1998; 98WO-US011927.  
 XX  
 PR 13-JUN-1997; 97US-00874807.  
 XX  
 PR 14-MAY-1998; 98US-00079030.  
 XX  
 PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
 XX  
 PI Guevara JG, Hoogetveen RC, Moore JP;  
 XX  
 DR WPI; 1999-070331/06.  
 XX  
 PT Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -  
 PT used for delivering nucleic acid to cells for gene therapy and antisense  
 XX treatment.  
 PS Claim 16; Fig 12C; 293pp; English.  
 XX  
 CC AAM96827-77 represent nucleic acid binding domains derived from human



OY 1 TTRLTRKRGK 11  
DB 5 TTRLTRKRGK 15

## RESULT 11

ABB37687  
ID ABB37687 standard; peptide; 343 AA.  
XX  
AC ABB37687;  
XX  
DT 04-FEB-2002 (first entry)  
XX  
DE Peptide #5193 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.  
OS Homo sapiens.

PN WO200157277-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000669.

PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-483447/52.

PT Human genome-derived single exon nucleic acid probes useful for analyzing  
XX  
PT gene expression in human fetal liver.

PS Claim 27; SEQ ID NO 30322; 639pp + Sequence Listing; English.  
XX

CC The invention relates to a single exon nucleic acid probe for measuring  
CC human gene expression in a sample derived from human foetal liver. The  
CC single exon nucleic acid probes may be used for predicting, measuring and  
CC displaying gene expression in samples derived from human foetal liver. The  
CC present sequence is a peptide encoded by a single exon nucleic acid probe  
CC of the invention. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 343 AA;

Query Match 100.0%; Score 54; DB 4; Length 343;  
Best Local Similarity 100.0%; Pred. No. 0.065;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTRLTRKRGK 11  
DB 168 TTRLTRKRGK 178

## RESULT 12

ABG52504  
ID ABG52504 standard; peptide; 343 AA.  
XX  
AC ABG52504;  
XX  
DT 25-FEB-2003 (first entry)  
XX

DE Human liver peptide, SEQ ID No 31152.  
XX  
XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
XX hypercholesterolaemia; coronary heart disease.  
XX  
OS Homo sapiens.

PN WO200157273-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000664.

PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488898/53.  
XX

PT Human genome-derived single exon nucleic acid probes useful for analyzing  
XX  
PT gene expression in human adult liver.

PS Claim 27; SEQ ID NO 31152; 658pp; English.  
XX

CC The invention relates to a single exon nucleic acid probe (SENP) (I) for  
CC measuring human gene expression in a sample derived from human adult  
CC liver, comprising one of 13109 defined nucleotide sequences given in the  
CC specification (or complements/ fragments). The probe hybridises at high  
CC stringency to a nucleic acid molecule expressed in the human adult liver.  
CC (I) may be used for predicting, measuring and displaying gene expression  
CC in samples derived from human adult liver. The genes identified may be  
CC involved in genetic liver diseases such as cirrhosis,  
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
CC associated with coronary heart disease. ABG47348-ABG59930 represent human  
CC liver single exon encoded peptides of the invention. Note: The sequence  
CC information for this patent does not appear in the printed specification  
CC but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 343 AA;

Query Match 100.0%; Score 54; DB 4; Length 343;  
Best Local Similarity 100.0%; Pred. No. 0.065;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTRLTRKRGK 11  
DB 168 TTRLTRKRGK 178

## RESULT 13

AAR72704  
ID AAR72704 standard; protein; 377 AA.  
XX  
AC AAR72704;  
XX  
DT 31-OCT-1995 (first entry)  
XX  
DE Human apo B-100 polypeptide 89.  
XX  
KW Apo B-100; hybridoma MB47; LDL cholesterol; low density lipoprotein;  
XX lipid.  
XX  
OS Homo sapiens.

XX

```

FH Key Location/Qualifiers
FT Peptide 1..377
FT /label= claimed
FT Peptide 140..297
FT /label= claimed
FT Peptide 173..297
FT /label= claimed
FT Peptide 205..297
FT /label= claimed
FT Peptide 216..377
FT /label= claimed
FT Peptide 216..352
FT /label= claimed
FT Peptide 216..331
FT /label= claimed
FT Peptide 216..310
FT /label= claimed
FT Peptide 216..310
FT /label= claimed
FT Peptide 217..297
FT /label= claimed
FT Peptide 217..297
FT /label= claimed
XX US5408038-A.
XX 18-APR-1995.
XX 08-OCT-1992; 92US-00959946.
XX 09-OCT-1991; 91US-00774633.
XX 18-JUN-1992; 92US-00901706.
XX (SCRI ) SCRIPPS RES INST.
XX Witztum JL, Koduri KR, Young SG, Smith RS, Curtiss LK;
XX MPI, 1993-134378/16.
XX N-PSDB; AAQ89633.
XX Polypeptide mimic of native apo B-100 and native apo A-I - useful in
XX assays for LDL and HDL in plasma samples.
XX Claim 6; Fig 1; 41pp; English.
XX AAQ89633 and AAR72704 depict the AA sequence of human apo B-100 and its
XX corresp. cDNA. From AA residue 3214 through residue 3590 according to the
XX numbering scheme of Ludwig et al., DNA, 6:363 (1987). Ludwig et al.
XX reported the full cDNA sequence for the human apo B-100 gene, consisting
XX of 29 exons. AAQ89633 corresp. to nt 9642-10770. The apo B-100 cDNA
XX segment in AAQ89633 encodes an apo B-100 polypeptide called s9. Other
XX truncated AA sequences and cDNA sequences of apo B-100 identified in the
XX disclosure are: No. N terminus C terminus AA nt AA nt s1 3429 10287 3510
XX 10530 82 3418 10254 3510 10530 83 3386 10158 3510 10530 84 3353 10059
XX 3510 10530 85 3429 10287 3523 10569 86 3429 10287 3544 10632 87 3429
XX 10287 3565 10695 88 3429 10287 3590 10770 89 3214 9642 3590 10770 Forward
XX (F) and reverse (R) primers that can be used to generate a cDNA segment
XX coding for the above fragments are given in AAQ86935- AAQ86944. A
XX polypeptide is claimed which comprises an AA sequence of Apo B-100 of up
XX to 375 residues and which includes residues 217-297 and which
XX immunoreacts with antibodies generated by the hybridoma MB47 having ATCC
XX Accession No. HB 8746. Claimed polypeptides are listed in FT. A fusion
XX polypeptide is also claimed which comprises a sequence of apo A-I (see
XX AAQ89634/R72705) and a sequence of apo B-100
XX
SQ Sequence 377 AA;
Query Match 100.0%; Score 54; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTRLTRKRGK 11
DB 144 TTRLTRKRGK 154

```

```

RESULT 14
AAR34031 standard; protein; 377 AA.
XX AAR34031;
XX AC AAR34031;
XX DT 25-MAR-2003 (revised)
XX DT 13-AUG-1993 (first entry)
XX DE Sequence of apo B-100.
XX KW Lipoprotein; apoprotein; B-100; A-I; LDL; HDL; assay.
XX OS Homo sapiens.
XX PN WO9307165-A1.
XX PD 15-APR-1993.
XX PF 09-OCT-1992; 92WO-US008634.
XX PR 09-OCT-1991; 91US-00774633.
XX PR 18-JUN-1992; 92US-00901706.
XX PR 08-OCT-1992; 92US-00959946.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Smith RS, Curtiss LK, Koduri KR, Witztum JL, Young SG;
XX MPI, 1993-134378/16.
XX DR N-PSDB; AAQ40029.
XX PT Polypeptide mimic of native apo B-100 and native apo A-I - useful in
XX assays for LDL and HDL in plasma samples.
XX PS Claim 6; Page 103-104; 137pp; English.
XX CC The inventors claim a portion of the polypeptide contg. apo B-100 that
XX CC immunoreacts with antibodies secreted by the hybridoma MB47 having ATCC
XX CC Accession No. 8746. Polypeptides specifically claimed include residues
XX CC 217-297, 216-310, 216-331, 216-352, 216-377, 1-377, 205-297, 173-297, 140
XX CC -297. DNA sequences encoding the polypeptides are also claimed. Also
XX CC claimed are a fusion polypeptide that contains: (a) a first amino
XX CC acid residue sequence up to 250 residues in length that includes residues
XX CC 120-135 of apo A-I, (b) a second amino acid residue sequence up to 375
XX CC residues in length that includes residues 217-297 of apo B-100 and DNA
XX CC encoding it. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25
XX CC -MAR-2003 to correct PR field.)
XX SQ Sequence 377 AA;
Query Match 100.0%; Score 54; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTRLTRKRGK 11
DB 144 TTRLTRKRGK 154
RESULT 15
ADJ57400 standard; protein; 2463 AA.
XX ADJ57400;
XX AC ADJ57400;
XX DT 06-MAY-2004 (first entry)
XX DE Human apolipoprotein B, marker for hepatocellular carcinoma.
XX DE Hepatocellular carcinoma; marker; human; apolipoprotein B; diagnosis.
XX KW
XX

```

```

OS Homo sapiens.
XX
PN WO2004005466-A2.
XX
PD 15-JAN-2004.
XX
PF 03-JUL-2003; 2003WO-US020841.
XX
PR 03-JUL-2002; 2002US-0393982P.
XX
PA (ILLU-) ILLUMIGEN BIOSCIENCES INC.
PI Katze M, Bumgarner R, Smit M, Rosenberg G;
XX
DR WPI; 2004-142977/14.
DR GENBANK; NP_000375.
XX
PT Detecting hepatocellular carcinoma (HCC) in mammals comprises obtaining
PT and assaying a biological sample to quantify a cell-associated or a non-
PT cell-associated HCC-related protein and comparing the quantity to a
PT control level.
XX
PS Disclosure; SEQ ID NO 4; 48bp; English.
XX
CC The present sequence is that of human apolipoprotein B. This non-cell
CC associated protein is one of a set of proteins characterised as
CC diagnostic targets for hepatocellular carcinoma (HCC). Such proteins are
CC the products of genes identified by expression microarray analysis of
CC tumour samples from hepatitis C virus (HCV) infected patients with HCC as
CC being specifically up-regulated in HCC tumour tissue when compared to HCV
CC infected cirrhotic non-tumour tissue and normal liver. The invention
CC relates to the detection of HCC by assaying patient samples such as
CC tissue, plasma, serum, etc. for the presence and level of specific HCC
CC related proteins. A finding of elevated levels of one or more of these
CC proteins in a patient sample indicates that the patient has HCC. Methods
CC for the diagnosis of HCC are provided, as well as improved assay methods
CC and scanning methods that employ non-cell-associated and cell-associated
CC HCC-related proteins.
XX
SQ Sequence 2463 AA;

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Query Match 100.0%; Score 54; DB 8; Length 2463;  
 Best Local Similarity 100.0%; Pred. No. 0.45;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TTRLTRRKGIX 11
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Db 1284 TTRLTRRKGIX 1294

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Search completed: January 12, 2005, 13:25:40  
 Job time : 102.484 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2005, 13:14:21 ; Search time 25.9032 Seconds  
(without alignments)  
28.162 Million cell updates/sec

Title: US-10-657-404a-2  
Perfect score: 54  
Sequence: 1 TTRLTRKRGK 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/6C.COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfilest.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	11	4	US-09-269-533A-2
2	54	100.0	13	4	US-09-269-533A-4
3	54	100.0	15	4	US-09-079-030-205
4	54	100.0	22	4	US-09-269-533A-5
5	54	100.0	22	4	US-09-269-533A-6
6	54	100.0	36	4	US-09-079-030-166
7	54	100.0	51	4	US-09-079-030-98
8	54	100.0	377	1	US-07-959-946-1
9	54	100.0	377	1	US-08-333-577-1
10	54	100.0	377	5	PCT-US92-08634-1
11	54	100.0	420	4	US-09-079-030-223
12	54	100.0	840	4	US-09-079-030-214
13	54	100.0	4536	4	US-09-180-422B-27
14	54	100.0	4536	4	US-09-079-030-1
15	54	100.0	4563	4	US-09-108-006C-1
16	54	100.0	4563	4	US-09-538-092-842
17	50	92.6	773	4	US-09-079-030-215
18	49	90.7	15	4	US-09-265-222-20
19	49	90.7	15	4	US-09-180-422B-17
20	45	83.3	10	4	US-09-265-222-1
21	45	83.3	10	4	US-09-265-222-6
22	44	81.5	10	4	US-09-265-222-5
23	44	81.5	10	4	US-09-265-222-7
24	44	81.5	10	4	US-09-265-222-9
25	44	81.5	10	4	US-09-265-222-11
26	44	81.5	11	4	US-09-269-533A-3
27	44	81.5	12	4	US-09-180-422B-13

## ALIGNMENTS

28	44	81.5	15	3	US-08-981-122-85	Sequence 85, Appl
29	44	81.5	785	4	US-09-079-030-216	Sequence 216, App
30	43	79.6	10	4	US-09-265-222-2	Sequence 2, Appl1
31	43	79.6	10	4	US-09-265-222-3	Sequence 3, Appl1
32	43	79.6	10	4	US-09-265-222-4	Sequence 4, Appl1
33	42	77.8	10	4	US-09-265-222-8	Sequence 8, Appl1
34	42	77.8	10	4	US-09-265-222-10	Sequence 10, Appl
35	42	77.8	10	4	US-09-265-222-12	Sequence 12, Appl
36	40	74.1	336	4	US-09-489-039A-13630	Sequence 13630, A
37	38.5	71.3	11	4	US-09-265-222-16	Sequence 16, Appl
38	38.5	71.3	11	4	US-09-265-222-17	Sequence 17, Appl
39	38.5	71.3	11	4	US-09-265-222-18	Sequence 18, Appl
40	38.5	71.3	11	4	US-09-265-222-19	Sequence 19, Appl
41	36	66.7	316	4	US-09-543-681A-4590	Sequence 4590, Ap
42	35	64.8	124	4	US-09-732-210-693	Sequence 693, App
43	35	64.8	390	3	US-09-108-020-36	Sequence 36, Appl
44	35	64.8	390	4	US-09-901-151-5	Sequence 5, Appl1
45	35	64.8	390	4	US-09-901-151-6	Sequence 6, Appl1

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RESULT 1
US-09-269-533A-2
; Sequence 2, Application US/09269533A
; Patent No. 6670452
; GENERAL INFORMATION:
; APPLICANT: University of Strathclyde
; APPLICANT: Halbert, Gavin
; APPLICANT: Owens, Moira
; APPLICANT: Bailly, George
; TITLE OF INVENTION: No. 6670452-Naturally Occurring Lipoprotein Particle
; FILE REFERENCE: P07885US
; CURRENT APPLICATION NUMBER: US/09/269,533A
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: PCT/GB97/02610
; PRIOR FILING DATE: 1997-09-25
; PRIOR APPLICATION NUMBER: GB 9620153.8
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent version 3.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..7)
; OTHER INFORMATION: Apo B binding site sequence
US-09-269-533A-2
Query Match 100.0%; Score 54; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTRLTRKRGK 11
Db 1 TTRLTRKRGK 11
RESULT 2
US-09-269-533A-4
; Sequence 4, Application US/09269533A
; Patent No. 6670452
; GENERAL INFORMATION:
; APPLICANT: University of Strathclyde
; APPLICANT: Halbert, Gavin
; APPLICANT: Owens, Moira
; APPLICANT: Bailly, George
; TITLE OF INVENTION: No. 6670452-Naturally Occurring Lipoprotein Particle
; FILE REFERENCE: P07885US
; CURRENT APPLICATION NUMBER: US/09/269,533A
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/ CURRENT FILING DATE: 1999-06-01
/ PRIOR APPLICATION NUMBER: PCT/GB97/02610
/ PRIOR FILING DATE: 1997-09-25
/ PRIOR APPLICATION NUMBER: GB 9620153.8
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1..7)
/ OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
/ NAME/KEY: misc.feature
/ LOCATION: (1..7)
/ OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
US-09-269-533A-4
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## Query Match

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Best Local Similarity 100.0%; Score 54; DB 4; Length 13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TTRLTRRRGK 11
Db 2 TTRLTRRRGK 12
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## RESULT 3

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US-09-079-030-205
/ Sequence 205, Application US/09079030
/ Patent No. 6635623
/ GENERAL INFORMATION:
/ APPLICANT: Guevera, Jr., Juan G.
/ APPLICANT: Hoogeveen, Ron C.
/ APPLICANT: Moore, Paul J.
/ TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
/ TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
/ NUMBER OF SEQUENCES: 229
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: USA
/ ZIP: 77210
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/079,030
/ FILING DATE: Concurrently Herewith
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McMillian, Nabeela R.
/ REGISTRATION NUMBER: P-43,363
/ REFERENCE/DOCKET NUMBER: ARAG:003
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512/474-7577
/ TELEFAX: 512/474-7577
/ INFORMATION FOR SEQ ID NO: 205:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
US-09-079-030-205
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Query Match 100.0%; Score 54; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00065;
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTRLTRRRGK 11
Db 5 TTRLTRRRGK 15
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## RESULT 4

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US-09-269-533A-5
/ Sequence 5, Application US/09269533A
/ Patent No. 6670452
/ GENERAL INFORMATION:
/ APPLICANT: University of Strathclyde
/ APPLICANT: Halbert, Gavin
/ APPLICANT: Owens, Moira
/ APPLICANT: Baillie, George
/ TITLE OF INVENTION: No. 6670452-Naturally Occurring Lipoprotein Particle
/ FILE REFERENCE: P0788505
/ CURRENT APPLICATION NUMBER: US/09/269,533A
/ PRIOR FILING DATE: 1999-06-01
/ PRIOR APPLICATION NUMBER: PCT/GB97/02610
/ PRIOR FILING DATE: 1997-09-25
/ PRIOR APPLICATION NUMBER: GB 9620153.8
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 5
/ LENGTH: 22
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1..7)
/ OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
/ NAME/KEY: misc.feature
/ LOCATION: (1..7)
/ OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue
/ NAME/KEY: misc.feature
/ LOCATION: (1..7)
/ OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
US-09-269-533A-5
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Query Match 100.0%; Score 54; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.00095;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 TTRLTRRRGK 11
Db 6 TTRLTRRRGK 16
```

## RESULT 5

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US-09-269-533A-6
/ Sequence 6, Application US/09269533A
/ Patent No. 6670452
/ GENERAL INFORMATION:
/ APPLICANT: University of Strathclyde
/ APPLICANT: Halbert, Gavin
/ APPLICANT: Owens, Moira
/ APPLICANT: Baillie, George
/ TITLE OF INVENTION: No. 6670452-Naturally Occurring Lipoprotein Particle
/ FILE REFERENCE: P0788505
/ CURRENT APPLICATION NUMBER: US/09/269,533A
/ PRIOR FILING DATE: 1999-06-01
/ PRIOR APPLICATION NUMBER: PCT/GB97/02610
/ PRIOR FILING DATE: 1997-09-25
/ PRIOR APPLICATION NUMBER: GB 9620153.8
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 6
/ LENGTH: 22
/ TYPE: PRT
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ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1..7)  
OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site  
NAME/KEY: misc feature  
LOCATION: (1..7)  
OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue  
US-09-269-533A-6

Query Match 100.0%; Score 54; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.00095;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11  
Db 6 TTRLTRKRGK 16

RESULT 6  
US-09-079-030-166  
Sequence 166, Application US/09079030  
Patent No. 6635623  
GENERAL INFORMATION:  
APPLICANT: Guevera, Jr., Juan G.  
APPLICANT: Hooogeveen, Ron C.  
APPLICANT: Moore, Paul J.  
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY  
NUMBER OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS  
NUMBER OF SEQUENCES: 229  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,030  
FILING DATE: Concurrently Herewith  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMillian, Nabeela R.  
REGISTRATION NUMBER: P-43,363  
REFERENCE/DOCKET NUMBER: ARAG:003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 166:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-09-079-030-166

Query Match 100.0%; Score 54; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11  
Db 10 TTRLTRKRGK 20

RESULT 7  
US-09-079-030-98  
Sequence 98, Application US/09079030

Patent No. 6635623  
GENERAL INFORMATION:  
APPLICANT: Guevera, Jr., Juan G.  
APPLICANT: Hooogeveen, Ron C.  
APPLICANT: Moore, Paul J.  
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY  
NUMBER OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS  
NUMBER OF SEQUENCES: 229  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,030  
FILING DATE: Concurrently Herewith  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMillian, Nabeela R.  
REGISTRATION NUMBER: P-43,363  
REFERENCE/DOCKET NUMBER: ARAG:003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 98:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 51 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-09-079-030-98

Query Match 100.0%; Score 54; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11  
Db 5 TTRLTRKRGK 15

RESULT 8  
US-07-959-946-1  
Sequence 1, Application US/07959946  
Patent No. 5408038  
GENERAL INFORMATION:  
APPLICANT: Smith, Richard K.  
APPLICANT: Koduri, Raju  
APPLICANT: Young, Stephen G.  
APPLICANT: Witzum, Joseph L.  
APPLICANT: Curtiss, Linda K.  
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a  
NUMBER OF INVENTION: Pan Native Epitope and Recombinant Antigens  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dressler, Goldsmith, Shore, Sucker &  
ADDRESS: Malinow, Ltd.  
STREET: 180 No. 5408038th Stetson, Suite 4700  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/07/959,946
  FILING DATE: 19921008
  CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 435
    FILING DATE: 18-JUN-1992
  ATTORNEY/AGENT INFORMATION:
    NAME: Gamsen, Edward P.
    REGISTRATION NUMBER: 29,381
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (312)616-5400
      TELEFAX: (312)616-5460
  INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 377 amino acids
      TYPE: AMINO ACID
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      US-07-959-946-1

Query Match
Best Local Similarity 100.0%; Score 54; DB 1; Length 377;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11
Db 144 TTRLTRKRGK 154

RESULT 9
US-08-333-577-1
Sequence 1, Application US/08333577
Patent No. 5786206
GENERAL INFORMATION:
  APPLICANT: Smith, Richard K.
  APPLICANT: Koduri, Raju
  APPLICANT: Young, Stephen G.
  APPLICANT: Witzum, Joseph L.
  APPLICANT: Curtiss, Linda K.
  TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
  NUMBER OF SEQUENCES: Pan Native Epitope and Recombinant Antigens
  CORRESPONDENCE ADDRESS:
    ADDRESSER: Dressler, Goldsmith, Shore, Suter &
    STREET: 180 No. 5786206th Stetson, Suite 4700
    CITY: Chicago
    STATE: Illinois
    COUNTRY: USA
    ZIP: 60601
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patent in Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/333,577
    FILING DATE:
  CLASSIFICATION:
    ATTORNEY/AGENT INFORMATION:
      NAME: Gamsen, Edward P.
      REGISTRATION NUMBER: 29,381
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: (312)616-5400
        TELEFAX: (312)616-5460
  INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 377 amino acids
      TYPE: amino acid

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; MOLECULE TYPE: protein
US-08-333-577-1

Query Match
Best Local Similarity 100.0%; Score 54; DB 1; Length 377;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11
Db 144 TTRLTRKRGK 154

RESULT 10
PCT-US92-08634-1
Sequence 1, Application PC/TUS9208634
GENERAL INFORMATION:
  APPLICANT: Smith, Richard K.
  APPLICANT: Koduri, Raju
  APPLICANT: Young, Stephen G.
  APPLICANT: Witzum, Joseph L.
  APPLICANT: Curtiss, Linda K.
  TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
  NUMBER OF SEQUENCES: Pan Native Epitope and Recombinant Antigens
  CORRESPONDENCE ADDRESS:
    ADDRESSER: Dressler, Goldsmith, Shore, Suter &
    STREET: 180 North Stetson, Suite 4700
    CITY: Chicago
    STATE: Illinois
    COUNTRY: USA
    ZIP: 60601
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patent in Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: PCT/US92/08634
    FILING DATE: 19921009
  CLASSIFICATION:
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/901,706
      FILING DATE: 18-JUN-1992
    ATTORNEY/AGENT INFORMATION:
      NAME: Gamsen, Edward P.
      REGISTRATION NUMBER: 29,381
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: (312)616-5400
        TELEFAX: (312)616-5460
  INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 377 amino acids
      TYPE: AMINO ACID
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      PCT-US92-08634-1

Query Match
Best Local Similarity 100.0%; Score 54; DB 5; Length 377;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11
Db 144 TTRLTRKRGK 154

RESULT 11
US-09-079-030-223
Sequence 223, Application US/09079030
Patent No. 6635623

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GENERAL INFORMATION:  
APPLICANT: Guevera, Jr., Juan G.  
APPLICANT: Hoogveen, Ron C.  
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY  
TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS  
NUMBER OF SEQUENCES: 229  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,030  
FILING DATE: Concurrently Herewith  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMillian, Nabehla R.  
REGISTRATION NUMBER: P-43,363  
REFERENCE/DOCKET NUMBER: ARAG:003  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 223:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 420 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-09-079-030-223

Query Match 100.0%; Score 54; DB 4; Length 420;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTLTRKRGK 11  
Db 57 TTTLTRKRGK 67

RESULT 12  
US-09-079-030-214  
Sequence 214 Application US/09079030  
Patent No. 6635623  
GENERAL INFORMATION:  
APPLICANT: Guevera, Jr., Juan G.  
APPLICANT: Hoogveen, Ron C.  
APPLICANT: Moore, Paul J.  
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY  
TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS  
NUMBER OF SEQUENCES: 229  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,030  
FILING DATE: Concurrently Herewith

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMillian, Nabehla R.  
REGISTRATION NUMBER: P-43,363  
REFERENCE/DOCKET NUMBER: ARAG:003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 214:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-09-079-030-214

Query Match 100.0%; Score 54; DB 4; Length 840;  
Best Local Similarity 100.0%; Pred. No. 0.037;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTLTRKRGK 11  
Db 657 TTTLTRKRGK 667

RESULT 13  
US-09-180-422B-27  
Sequence 27 Application US/09180422B  
Patent No. 6444644  
GENERAL INFORMATION:  
APPLICANT: BRUCKDORFER, KARL R  
TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED  
FROM APOLIPOPROTEIN B-100  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE, P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/180,422B  
FILING DATE: 07-Dec-1998  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36663  
REFERENCE/DOCKET NUMBER: 117-268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164000  
TELEFAX: 7038164100  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4536 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-180-422B-27

Query Match 100.0%; Score 54; DB 4; Length 4536;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTLTRKRGK 11

Db 3357 TTRLTRKRGK 3367

RESULT 14  
US-09-079-030-1

Sequence 1, Application US/09079030  
Patent No. 6635623

GENERAL INFORMATION:

APPLICANT: Guevera, Jr., Juan G.  
APPLICANT: Hoogeveen, Ron C.

TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY

NUMBER OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS

CORRESPONDENCE ADDRESS: 229

ADDRESSER: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/079,030

FILING DATE: Concurrently Herewith

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: McWilliam, Nabeela R.

REGISTRATION NUMBER: P-43,363

REFERENCE/DOCKET NUMBER: ARAG:003

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4536 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-09-079-030-1

Query Match

Best Local Similarity 100.0%; Score 54; DB 4; Length 4536;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTRLTRKRGK 11

Db 3357 TTRLTRKRGK 3367

RESULT 15

US-09-108-006C-1

Sequence 1, Application US/09108006C

Patent No. 6524613

GENERAL INFORMATION:

APPLICANT: Steer, Clifford J.

Kren, Betsy T.

Bandyopadhyay, Paramita

Roy-Chowdhury, Jayanta

TITLE OF INVENTION: Hepatocellular Chimera

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSER: Kimeragen, Inc.

STREET: 300 Pleasant Run

CITY: Newtown

STATE: PA

COUNTRY: USA

ZIP: 18940

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/108,006C

FILING DATE: 30-Jun-1992

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/054,288

FILING DATE: 30-Apr-1997

APPLICATION NUMBER: 60/054,837

FILING DATE: 05-Aug-1997

APPLICATION NUMBER: 60/064,996

FILING DATE: 10-Nov-1997

APPLICATION NUMBER: 60/074,497

FILING DATE: 12-Feb-1998

APPLICATION NUMBER: PCT US 98/08834

FILING DATE: 30-Apr-1998

ATTORNEY/AGENT INFORMATION:

NAME: Friedel, Thomas

REGISTRATION NUMBER: 29258

REFERENCE/DOCKET NUMBER: 7991-015-999

TELEPHONE: 215-504-4444

TELEFAX: 215-504-4545

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4563 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-108-006C-1

Query Match

Best Local Similarity 100.0%; Score 54; DB 4; Length 4563;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTRLTRKRGK 11

Db 3384 TTRLTRKRGK 3394

Search completed: January 12, 2005, 13:33:16  
Job time : 26.9032 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: January 12, 2005, 13:31:02 ; Search time 88.3548 Seconds  
(without alignments)  
44.980 Million cell updates/sec

Title: US-10-657-404A-2  
Perfect score: 54  
Sequence: 1 TTRLTRKRGK 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues  
Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10A\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	11	9	US-09-269-533A-2
2	54	100.0	11	17	US-10-657-404A-2
3	54	100.0	13	9	US-09-269-533A-4
4	54	100.0	13	17	US-10-657-404A-4
5	54	100.0	22	9	US-09-269-533A-5
6	54	100.0	22	9	US-09-269-533A-6
7	54	100.0	22	17	US-10-657-404A-5
8	54	100.0	22	17	US-10-657-404A-6
9	54	100.0	25	17	US-10-657-404A-9
10	54	100.0	34	15	US-10-333-313-1
11	54	100.0	343	9	US-09-864-761-46837
12	54	100.0	3000	16	US-10-741-601-431
13	54	100.0	4563	9	US-09-870-759-128

14	54	100.0	4563	10	US-09-802-640-32	Sequence 32, Appl
15	54	100.0	4563	10	US-09-751-708A-128	Sequence 128, App
16	54	100.0	4563	14	US-10-403-902A-32	Sequence 32, Appl
17	54	100.0	4563	16	US-10-741-601-432	Sequence 432, App
18	54	100.0	4563	16	US-10-741-601-433	Sequence 433, App
19	54	100.0	4563	17	US-10-428-817A-124	Sequence 124, App
20	49	90.7	10	9	US-09-823-418-20	Sequence 20, Appl
21	49	90.7	10	9	US-09-822-965-20	Sequence 20, Appl
22	45	83.3	10	9	US-09-823-418-1	Sequence 1, Appl
23	45	83.3	10	9	US-09-823-418-6	Sequence 6, Appl
24	45	83.3	10	9	US-09-822-965-1	Sequence 1, Appl
25	45	83.3	10	9	US-09-822-965-6	Sequence 6, Appl
26	45	83.3	10	10	US-09-572-404B-595	Sequence 595, App
27	45	83.3	10	10	US-09-572-404B-635	Sequence 635, App
28	45	83.3	10	10	US-09-572-404B-729	Sequence 729, App
29	44	81.5	9	17	US-10-657-404A-8	Sequence 8, Appl
30	44	81.5	10	9	US-09-823-418-7	Sequence 7, Appl
31	44	81.5	10	9	US-09-823-418-9	Sequence 9, Appl
32	44	81.5	10	9	US-09-823-418-11	Sequence 11, Appl
33	44	81.5	10	9	US-09-822-965-5	Sequence 5, Appl
34	44	81.5	10	9	US-09-822-965-7	Sequence 7, Appl
35	44	81.5	10	9	US-09-822-965-9	Sequence 9, Appl
36	44	81.5	10	9	US-09-822-965-11	Sequence 11, Appl
37	44	81.5	10	9	US-09-269-533A-3	Sequence 3, Appl
38	44	81.5	11	9	US-09-398-902-2	Sequence 2, Appl
39	44	81.5	11	9	US-09-931-375A-76	Sequence 76, Appl
40	44	81.5	11	10	US-10-358-594-2	Sequence 2, Appl
41	44	81.5	11	14	US-10-657-404A-3	Sequence 3, Appl
42	44	81.5	11	17	US-09-823-418-2	Sequence 2, Appl
43	44	79.6	10	9	US-09-823-418-3	Sequence 3, Appl
44	44	79.6	10	9	US-09-823-418-4	Sequence 4, Appl
45	43	79.6	10	9	US-09-823-418-4	Sequence 4, Appl

#### ALIGNMENTS

RESULT 1  
US-09-269-533A-2  
Sequence 2, Application US/09269533A  
Patent No. US20020147304A1  
GENERAL INFORMATION:  
APPLICANT: University of Strathclyde  
APPLICANT: Halbert, Gavin  
APPLICANT: Owens, Maira  
TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle  
FILE REFERENCE: P07885US  
CURRENT APPLICATION NUMBER: US/09/269, 533A  
CURRENT FILING DATE: 1999-06-01  
PRIOR APPLICATION NUMBER: PCT/GB97/02610  
PRIOR FILING DATE: 1997-09-25  
PRIOR APPLICATION NUMBER: GB 9620153.8  
PRIOR FILING DATE: 1996-09-27  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1..7)  
OTHER INFORMATION: Apo B binding site sequence  
US-09-269-533A-2  
Query Match 100.0%; Score 54; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0032; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0;  
Cv 1 TTRLTRKRGK 11  
Db 1 TTRLTRKRGK 11

## RESULT 2

US-10-657-404A-2  
; Sequence 2, Application US/10657404A  
; Publication No. US20040235730A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Strathclyde  
; APPLICANT: Halbert, Gavin  
; APPLICANT: Owens, Moira  
; TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle  
; FILE REFERENCE: P07885US-CIP  
; CURRENT APPLICATION NUMBER: US/10/657,404A  
; PRIOR FILING DATE: 2003-09-08  
; PRIOR APPLICATION NUMBER: PCT/GB97/02610  
; PRIOR FILING DATE: 1997-09-25  
; PRIOR APPLICATION NUMBER: GB 9620153.8  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Apo B binding site sequence  
US-10-657-404A-2

## Query Match

Best Local Similarity 100.0%; Score 54; DB 17; Length 11;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRRGGK 11  
Db 1 TTRLTRRGGK 11

## RESULT 3

US-09-269-533A-4  
; Sequence 4, Application US/09269533A  
; Patent No. US20020147304A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Strathclyde  
; APPLICANT: Halbert, Gavin  
; APPLICANT: Owens, Moira  
; TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle  
; FILE REFERENCE: P07885US  
; CURRENT APPLICATION NUMBER: US/09/269,533A  
; PRIOR FILING DATE: 1999-06-01  
; PRIOR APPLICATION NUMBER: PCT/GB97/02610  
; PRIOR FILING DATE: 1997-09-25  
; PRIOR APPLICATION NUMBER: GB 9620153.8  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (..T)  
; OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site  
; NAME/KEY: misc feature  
; LOCATION: (..T)  
; OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue  
US-09-269-533A-4

## Query Match

Best Local Similarity 100.0%; Score 54; DB 9; Length 13;  
Matches 100.0%; Pred. No. 0.0038;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRRGGK 11  
Db 2 TTRLTRRGGK 12

## RESULT 4

US-10-657-404A-4  
; Sequence 4, Application US/10657404A  
; Publication No. US20040235730A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Strathclyde  
; APPLICANT: Halbert, Gavin  
; APPLICANT: Owens, Moira  
; TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle  
; FILE REFERENCE: P07885US-CIP  
; CURRENT APPLICATION NUMBER: US/10/657,404A  
; PRIOR FILING DATE: 2003-09-08  
; PRIOR APPLICATION NUMBER: PCT/GB97/02610  
; PRIOR FILING DATE: 1997-09-25  
; PRIOR APPLICATION NUMBER: GB 9620153.8  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue  
US-10-657-404A-4

## Query Match

Best Local Similarity 100.0%; Score 54; DB 17; Length 13;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRRGGK 11  
Db 2 TTRLTRRGGK 12

## RESULT 5

US-09-269-533A-5  
; Sequence 5, Application US/09269533A  
; Patent No. US20020147304A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Strathclyde  
; APPLICANT: Halbert, Gavin  
; APPLICANT: Owens, Moira  
; TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle  
; FILE REFERENCE: P07885US  
; CURRENT APPLICATION NUMBER: US/09/269,533A  
; PRIOR FILING DATE: 1999-06-01  
; PRIOR APPLICATION NUMBER: PCT/GB97/02610  
; PRIOR FILING DATE: 1997-09-25  
; PRIOR APPLICATION NUMBER: GB 9620153.8  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (..T)

OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site  
NAME/KEY: misc feature  
LOCATION: (1..1)  
OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue  
NAME/KEY: misc feature  
LOCATION: (1..1)  
OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue  
US-09-269-533A-5

Query Match 100.0%; Score 54; DB 9; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.0065;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11  
Db 6 TTRLTRKRGK 16

RESULT 6  
US-09-269-533A-6

Sequence 6, Application US/09269533A  
Patent No. US20020147304A1  
GENERAL INFORMATION:  
APPLICANT: University of Strathclyde  
APPLICANT: Halbert, Gavin  
APPLICANT: Owens, Molra  
APPLICANT: Baillie, George  
TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle  
FILE REFERENCE: P07885US  
CURRENT APPLICATION NUMBER: US/09/269, 533A  
CURRENT FILING DATE: 1999-06-01  
PRIOR FILING DATE: 1997-09-25  
PRIOR APPLICATION NUMBER: PCT/GB97/02610  
PRIOR FILING DATE: 1996-09-27  
PRIOR APPLICATION NUMBER: GB 9620153.8  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 6  
LENGTH: 22  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1..1)  
OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site  
NAME/KEY: misc feature  
LOCATION: (1..1)  
OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue  
US-09-269-533A-6

Query Match 100.0%; Score 54; DB 9; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.0065;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11  
Db 6 TTRLTRKRGK 16

RESULT 7  
US-10-657-404A-5

Sequence 5, Application US/10657404A  
Publication No. US20040235730A1  
GENERAL INFORMATION:  
APPLICANT: University of Strathclyde  
APPLICANT: Halbert, Gavin  
APPLICANT: Owens, Molra  
APPLICANT: Baillie, George  
TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle  
FILE REFERENCE: P07885US-CIP  
CURRENT APPLICATION NUMBER: US/10/657, 404A  
CURRENT FILING DATE: 2003-09-08  
PRIOR APPLICATION NUMBER: PCT/GB97/02610

PRIOR FILING DATE: 1997-09-25  
PRIOR APPLICATION NUMBER: GB 9620153.8  
PRIOR FILING DATE: 1996-09-27  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 22  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site  
NAME/KEY: misc feature  
LOCATION: (1..1)  
OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue  
NAME/KEY: misc feature  
LOCATION: (1..1)  
OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue  
US-10-657-404A-5

Query Match 100.0%; Score 54; DB 17; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.0065;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11  
Db 6 TTRLTRKRGK 16

RESULT 8  
US-10-657-404A-6

Sequence 6, Application US/10657404A  
Publication No. US20040235730A1  
GENERAL INFORMATION:  
APPLICANT: University of Strathclyde  
APPLICANT: Halbert, Gavin  
APPLICANT: Owens, Molra  
APPLICANT: Baillie, George  
TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle  
FILE REFERENCE: P07885US-CIP  
CURRENT APPLICATION NUMBER: US/10/657, 404A  
CURRENT FILING DATE: 2003-09-08  
PRIOR FILING DATE: 1996-09-27  
PRIOR APPLICATION NUMBER: PCT/GB97/02610  
PRIOR FILING DATE: 1997-09-25  
PRIOR APPLICATION NUMBER: GB 9620153.8  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 22  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site  
NAME/KEY: misc feature  
LOCATION: (1..1)  
OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue  
US-10-657-404A-6

Query Match 100.0%; Score 54; DB 17; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.0065;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11  
Db 6 TTRLTRKRGK 16

RESULT 9  
US-10-657-404A-9

Sequence 9, Application US/10657404A  
Publication No. US20040235730A1

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/ GENERAL INFORMATION:
/ APPLICANT: University of Strathclyde
/ APPLICANT: Halbert, Gavin
/ APPLICANT: Owens, Moira
/ APPLICANT: Baillie, George
/ TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle
/ FILE REFERENCE: P07885US-CIP
/ CURRENT APPLICATION NUMBER: US/10/657,404A
/ PRIOR FILING DATE: 2003-09-08
/ PRIOR APPLICATION NUMBER: PCT/GB97/02610
/ PRIOR FILING DATE: 1997-09-25
/ PRIOR APPLICATION NUMBER: GB 9620153.8
/ PRIOR FILING DATE: 1996-09-27
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 9
/ LENGTH: 25
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
/ NAME/KEY: MISC FEATURE
/ OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ OTHER INFORMATION: Pyrene butyric acid linked at N-terminus of peptide analogue
US-10-657-404A-9
```

```
Query Match
Best Local Similarity 100.0%; Score 54; DB 17; Length 25;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 TTRLTRKRGK 11
DB 5 TTRLTRKRGK 15
```

```
RESULT 10
US-10-333-313-1
/ Sequence 1, Application US/10333313
/ Publication No. US20040091934A1
/ GENERAL INFORMATION:
/ APPLICANT: Narvaen, Outi
/ APPLICANT: Yla-Herttuala, Seppo
/ TITLE OF INVENTION: Peptides and Their Use in Assays for Cardiovascular Disease
/ FILE REFERENCE: GJE-6363
/ CURRENT APPLICATION NUMBER: US/10/333,313
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: PCT/GB01/03212
/ PRIOR FILING DATE: 2001-07-18
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 34
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: oligopeptide
US-10-333-313-1
```

```
Query Match
Best Local Similarity 100.0%; Score 54; DB 15; Length 34;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TTRLTRKRGK 11
DB 24 TTRLTRKRGK 34
```

```
RESULT 11
US-09-864-761-46837
/ Sequence 46837, Application US/09864761
```

```
/ Patent No. US20020048763A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ FILE REFERENCE: Aeonica-X-1
/ CURRENT APPLICATION NUMBER: US/09/864,761
/ PRIOR FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 46837
/ LENGTH: 343
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC010872.3
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.7
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 26
/ OTHER INFORMATION: EST HUMAN HIT: A1174984.1, EVALUATE 2.00e-60
/ OTHER INFORMATION: SWISSPROT HIT: P04114, EVALUATE 0.00e+00
US-09-864-761-46837
```

```
Query Match
Best Local Similarity 100.0%; Score 54; DB 9; Length 343;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TTRLTRKRGK 11
DB 168 TTRLTRKRGK 178
```

```
RESULT 12
US-10-741-601-431
/ Sequence 431, Application US/10741601
```

```

; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 431
; LENGTH: 3000
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-741-601-431

```

Query Match	100.0%	Score 54	DB 16	Length 3000
Best Local Similarity	100.0%	Pred. No.	0.88	
Matches	11	Conservative	0	Indels 0
		Mismatches	0	Gaps 0

OY	1	TTRLTRKGLK	11
Db	2336	TTRLTRKGLK	2346

```

RESULT 13
US-09-870-759-128
; Sequence 128 Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TEWMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
; LENGTH: 4563
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-128

```

Query Match	100.0%	Score 54	DB 9	Length 4563
Best Local Similarity	100.0%	Pred. NC 1.3		
Matches 11	Conservative 0	Mismatches 0	Gaps 0	

QY	1	TTRLTRKRG	LK	11
Db	3384	TTRLTRKRG	LK	3394

```

RESULT 14
US-09-802-640-32
; Sequence 32. Application US/09802640
; Publication NO. US20030036057A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bomsal Aruna
; APPLICANT: Kleya Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048
; CURRENT APPLICATION NUMBER: US/09/802,640
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 4563
; TYPE: PR1
; ORGANISM: Homo sapien

```

US-09-802-640-32

Query Match	100.0%;	Score 54;	DB 10;	Length 4563;
Best Local Similarity	100.0%;	Pred. No. 1.3;		
Matches 11;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	TTRLTRKRG	11
Db	3384	TTRLTRKRG	3394

```

, RESULT 15
, US-09-751-708A-128
, Sequence 128. Application US/09751708A
, Publication No. US20030157113A1
, GENERAL INFORMATION:
, APPLICANT: TERMAN, David S
, TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
, FILE REFERENCE: 751708
, CURRENT APPLICATION NUMBER: US/09/751,708A
, PRIORITY FILING DATE: 2002-10-15
, PRIOR APPLICATION NUMBER: US 60/173,371
, PRIORITY FILING DATE: 1999-12-28
, NUMBER OF SEQ ID NOS: 166
, SOFTWARE: PatentIn version 3.1
, SEQ ID NO 128
, LENGTH: 4563
, TYPE: PRT
, ORGANISM: Homo sapiens
, US-09-751-708A-128

```

	Query Match	100.0%	Score 54;	DB 10;	Length 4563;
	Best Local Similarity	Pred.	No. 1.3;		
	Matches    11;	Conservative	0;	Mismatches	0; Indels      0; Gaps     0;
Qy	1 TTRLTRRGGK 11				
Dz	3384 TTRLTRRGGK 3394				

Search completed: January 12, 2005, 13:52:50  
Job time : 89.3548 Secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 12, 2005, 13:13:31 ; Search time 20.2258 Seconds  
(without alignments)  
52.328 Million cell updates/sec

Title: US-10-657-404A-2  
Perfect score: 54  
Sequence: 1 TTRLTRKRGK 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	596	2 S32802	apolipoprotein B -
2	54	100.0	4563	1 LPHUB	apolipoprotein B-1
3	50	92.6	269	2 C60950	apolipoprotein B-1
4	50	92.6	779	2 JH0102	apolipoprotein B -
5	44	81.5	274	2 A60950	apolipoprotein B-1
6	44	81.5	275	2 B60950	apolipoprotein B-1
7	44	81.5	784	2 JH0101	apolipoprotein B-1
8	43	79.6	309	2 AH0906	conserved hypochet
9	41	75.9	309	1 B55112	hypothetical 34.6
10	41	75.9	309	2 B85985	hypothetical prote
11	41	75.9	309	2 B91140	hypothetical prote
12	38.5	71.3	2073	1 BMA582	bmg protein - Eme
13	38	70.4	1058	2 S55460	apolipoprotein B -
14	38	70.4	1778	2 J70382	apolipoprotein B -
15	38	70.4	2629	2 I46569	apolipoprotein B -
16	37	68.5	680	2 AB1875	hypothetical prote
17	36	66.7	146	2 T14681	myc-like regulator
18	36	66.7	590	2 E87337	ferrous iron trans
19	35	64.8	124	2 H64221	ribosomal protein
20	35	64.8	305	2 A75334	lacyl-carrier-prot
21	35	64.8	388	1 DEHUP7	pyruvate dehydrog
22	35	64.8	389	1 DEGPA	pyruvate dehydrog
23	35	64.8	390	1 DEHUPA	pyruvate dehydrog
24	35	64.8	390	1 DEHUPA	pyruvate dehydrog
25	35	64.8	390	1 DEHUPA	pyruvate dehydrog
26	35	64.8	390	2 S23506	pyruvate dehydrog
27	35	64.8	689	2 AC1408	transcription anti
28	35	64.8	689	2 AC1784	transcription anti
29	34	63.0	114	2 A90827	hypothetical prote

30	34	63.0	188	2 A87301	MutT/nudix family
31	34	63.0	191	2 E72480	hypothetical prote
32	34	63.0	300	2 AE3532	transposase BME110
33	34	63.0	309	2 AB3538	transposase BME110
34	34	63.0	325	2 T29604	hypothetical prote
35	34	63.0	393	2 S48288	probable phosphor
36	34	63.0	484	2 S40051	starch synthase (E
37	34	63.0	543	2 C66212	hypothetical prote
38	34	63.0	561	1 S34191	suflite reductase
39	34	63.0	857	2 T37459	ribonucleotide red
40	34	63.0	1232	2 T21018	hypothetical prote
41	33	61.1	107	2 S12607	salivary glue prot
42	33	61.1	112	2 S33822	hypothetical prote
43	33	61.1	198	2 T41525	hypothetical prote
44	33	61.1	219	2 A53305	pentose-5-phosphat
45	33	61.1	258	2 T01873	hypothetical prote

## ALIGNMENTS

## RESULT 1

S32802  
apolipoprotein B - crab-eating macaque (fragment)  
C:Species: Macaca fascicularis (crab-eating macaque)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S32802  
R:Pepe, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchic  
Biochim. Biophys. Acta 1086, 326-334, 1991  
A>Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional re  
A:Reference number: S32802; MUID:92075708; PMID:1742325  
A:Accession: S32802  
A>Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-596 <PAP>  
A:Cross-references: UNIPROT:Q28473; EMBL:X15737; NID:G38047; PIDN:CAA3755.1; PID:G93012  
C:Superfamily: apolipoprotein B

Query Match 100.0%; Score 54; DB 2; Length 596;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTRLTRKRGK 11  
DB 225 TTRLTRKRGK 235

## RESULT 2

LPHUB  
apolipoprotein B-100 precursor - human  
N:Contains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74  
C:Species: Homo sapiens (man)  
C>Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 09-Jul-2004  
C:Accession: A27850; A25679; A25263; A24330; A24684; A23817; A25774; A26  
4452; I61909; I59510; I39474; I39459; I84624; I37179; PS0058  
R:Rundwig, B.H.; Blackhart, B.D.; Pierotti, V.R.; Catali, L.; Fortier, C.; Knott, T.; Sco  
DNA 6, 363-372, 1987  
A>Title: DNA sequence of the human apolipoprotein B gene.  
A:Reference number: A27850; MUID:88003974; PMID:3652907  
A:Accession: A27850  
A:Molecule type: DNA  
A:Residues: 1-617, 'A', 619-1929, 'F', 1931-3318, 'D', 3320-3426, 'T', 3428-3431, 'Q', 3433-3721, '  
A:Cross-references: UNIPROT:P04114; UNIPROT:P78482; UNIPROT:P78479; UNIPROT:Q9UMN0; UNIP  
R:Cladaras, C.; Hadzopoulos-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.  
EMBO J. 5, 3495-3507, 1986  
A>Title: The complete sequence and structural analysis of human apolipoprotein B-100: re  
A:Reference number: A91058; MUID:87161758; PMID:3030729  
A:Accession: A25679  
A:Molecule type: mRNA  
A:Residues: 1-11, 15-2539, 'S', 2541-3823, 'R', 3825-4563 <CIA>  
A>Note: 1109-Abp was also found  
R:Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lueis, A.J.; Blackhart, B.; McCa  
Nucleic Acids Res. 14, 7501-7503, 1986

A/Title: Complete cDNA and derived protein sequence of human apolipoprotein B-100.  
A/Reference number: A93639; MUID:87016385; PMID:3763409  
A/Accession: A25263  
A/Molecule type: mRNA  
A/Residues: 1-272, 'N', 274-617, 'A', 619-1217, 'E', 1219-2091, 'V', 2093-2364, 'T', 2366-2679, 'Q'  
A/Cross-references: GB:040506; NID:934330; PIDN:CAA8191.1; PID:934331  
R/Law, S.W.; Grant, S.M.; Higuchi, K.; Hospattanakar, A.; Lackner, K.; Lee, N.; Brewer J.  
Proc. Natl. Acad. Sci. U.S.A. 83, 8142-8146, 1986  
A/Title: Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino  
A/Reference number: A94134; MUID:87041416; PMID:3464946  
A/Accession: A25267  
A/Molecule type: mRNA  
A/Residues: 1-617, 'A', 619-703, 'P', 705-792, 'R', 794-1270, 'S', 1272-1866, 'G', 1868-2036, 'N', 2  
4189-4220, 'W', 4222-4563, 'LAW>  
A/Note: The codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and  
J. Biol. Chem. 261, 12918-12921, 1986  
A/Title: The complete cDNA and amino acid sequence of human apolipoprotein B-100.  
A/Reference number: A92556; MUID:87008488; PMID:3759943  
A/Accession: A25266  
A/Molecule type: mRNA  
A/Residues: 1-97, 'I', 99-328, 'V', 330-644, 'I', 646-918, 'P', 920-3318, 'D', 3320-3426, 'T', 3428-  
9-4132, 'G', 4134-4180, 'E', 4182-4563, 'CH>  
A/Cross-references: GB:U02610; NID:9278803; PIDN:AAA5549.1; PID:9178804  
A/Note: A total of 2366 residues were confirmed by direct sequencing of tryptic peptides  
R/Procter, A.A.; Hardman, D.A.; Sato, K.Y.; Schilling, J.W.; Yamana, M.; Hori, Y.; H  
Proc. Natl. Acad. Sci. U.S.A. 83, 5678-5682, 1986  
A/Title: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein  
A/Reference number: A24320; MUID:86287319; PMID:3461454  
A/Accession: A24320  
A/Molecule type: mRNA  
A/Residues: 1-97, 'I', 99-617, 'A', 619-941, 'YYINSLPKP', 951-1138, 'PTGRLNCFSGNGLCYSLWHSQF  
A/Cross-references: GB:M14081; NID:9178795; PIDN:AAA51752.1; PID:9553189  
R/Law, S.W.; Lackner, K.J.; Hospattanakar, A.V.; Anchors, J.M.; Sakaguchi, A.Y.; Naylor,  
Proc. Natl. Acad. Sci. U.S.A. 82, 8340-8344, 1985  
A/Title: Human apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of  
A/Reference number: A24684; MUID:86094221; PMID:3001697  
A/Accession: A24684  
A/Molecule type: mRNA  
A/Residues: 485-617, 'A', 619-1044, 'LAW>  
A/Cross-references: GB:M12480; NID:9178791; PIDN:AAA51751.1; PID:9178792  
R/Procter, A.A.; Hardman, D.A.; Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; Ki  
Proc. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986  
A/Title: Isolation of a cDNA clone encoding the amino-terminal region of human apolipop  
A/Reference number: A94088; MUID:86193325; PMID:3513177  
A/Accession: A23817  
A/Molecule type: mRNA  
A/Residues: 1-291, 'PRO>  
A/Cross-references: GB:M12681; NID:9178797; PIDN:AAA51753.1; PID:9178798  
R/Deeb, S.S.; Motulsky, A.G.; Albers, J.J.  
Proc. Natl. Acad. Sci. U.S.A. 82, 4983-4986, 1985  
A/Title: A partial cDNA clone for human apolipoprotein B.  
A/Reference number: A25774; MUID:85270450; PMID:3860836  
A/Accession: A25774  
A/Molecule type: mRNA  
A/Residues: 709-791, 'SSSMKRAASGCHPSAGD', 810-906, 'DEB>  
A/Cross-references: GB:K03175; NID:9178821; PIDN:AAA51759.1; PID:9178822  
R/Carlsson, P.; Dairfjors, C.; Olofsson, S.O.; Bjurell, G.  
Gene 49, 29-51, 1986  
A/Title: Analysis of the human apolipoprotein B gene; complete structure of the B-74 reg  
A/Reference number: A91565; MUID:87191599; PMID:2883086  
A/Accession: A26533  
A/Molecule type: mRNA  
A/Residues: 1282-2721, 2742-3290, 'L', 3292-3336, 'N', 3338-3948, 'F', 3950-3963, 'Y', 3965-4180,  
A/Cross-references: GB:M15421; NID:9178817; PIDN:AAA51756.1; PID:9178818  
R/Hartman, D.A.; Procter, A.A.; Chen, G.C.; Schilling, J.W.; Sato, K.Y.; Lau, K.; Yamana  
Biochemistry 26, 5478-5486, 1987  
A/Title: Structural comparison of human apolipoproteins B-48 and B-100.  
A/Reference number: A29671; MUID:88050832; PMID:3676265  
A/Accession: A29671  
A/Molecule type: mRNA  
A/Residues: 1671-2323, 'PYW', 2327-2352, 'H', 2354-2398, 'HAR>  
A/Cross-references: GB:M17367; NID:9178731; PIDN:AAA51741.1; PID:9178732

R/Shoulders, C.C.; Myant, N.B.; Sidoti, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E.  
Atherosclerosis 58, 277-289, 1985  
A/Title: Molecular cloning of human LDL apolipoprotein B cDNA. Evidence for more than on  
A/Reference number: A90084; MUID:86130855; PMID:3841481  
A/Accession: A29287  
A/Molecule type: mRNA  
A/Residues: 3846-4298, 'SHO>  
R/Pfizenr, R.; Wagnere, R.; Stoffel, W.  
Biol. Chem. Hoppe-Seyler 367, 1077-1083, 1986  
A/Title: Isolation, expression and characterization of a human apolipoprotein B 100-spec  
A/Reference number: A25572; MUID:87076044; PMID:3024665  
A/Accession: A25572  
A/Molecule type: mRNA  
A/Residues: 4219-4337, 'S', 4339-4563, 'PFI>  
A/Cross-references: GB:M35676  
R/Mel, C.F.; Chen, S.H.; Yang, C.Y.; Marcel, Y.L.; Milne, R.W.; Li, W.H.; Sparrow, J.T.  
Proc. Natl. Acad. Sci. U.S.A. 82, 7265-7269, 1985  
A/Reference number: A24738; MUID:86042646; PMID:2932736  
A/Accession: A24738  
A/Molecule type: mRNA  
A/Residues: 'N', 3729-3731, 'I', 3733-3875, 'A', 3877-3948, 'P', 3950-3963, 'Y', 3965-3982, 'S', 39  
A/Cross-references: GB:M12413; NID:9178735; PIDN:AAA51742.1; PID:9178736  
R/Chen, S.H.; Habib, G.; Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silderman, S.R.; Cai  
Science 238, 363-366, 1987  
A/Title: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific li  
A/Reference number: A40133; MUID:88018019; PMID:3659919  
A/Accession: B40133  
A/Molecule type: mRNA  
A/Residues: 2165-2179, 'CHI>  
A/Cross-references: GB:M18036; NID:9178799; PIDN:AAA51754.1; PID:9178800  
A/Note: this mRNA includes the stop codon of the organ-specific mRNA for ap048  
A/Accession: A40133  
A/Molecule type: mRNA  
A/Residues: 51-75, 101-110, 129-139, 158-174, 197-207, 276-287, 298-304, 306-314, 526-532, 538-55  
36, 1486-1498, 1537-1556, 1553-1572, 1601-1610, 1647-1661, 1697-1724, 1770-1781, 1859-1897, 1968-  
A/Note: these fragments were derived from ap048  
R/Hartman, D.A.; Procter, A.A.; Schilling, J.W.; Kane, J.P.  
Biochem. Biophys. Res. Commun. 149, 1214-1219, 1987  
A/Title: Carboxyl terminal analysis of human B-48 protein confirms the novel mechanism p  
A/Reference number: A28002; MUID:88106542; PMID:3426612  
A/Accession: A28002  
A/Molecule type: mRNA  
A/Residues: 2129-2179, 2181-2235, 'HAN>  
A/Cross-references: GB:M18471  
A/Note: this mRNA from intestine includes a stop codon created by RNA editing in place o  
Nucleic Acids Res. 13, 6937-6953, 1985  
A/Title: Human apolipoprotein B: identification of cDNA clones and characterization of m  
A/Reference number: A24269; MUID:86041888; PMID:3903660  
A/Accession: A24269  
A/Molecule type: mRNA  
A/Residues: 3056-3159, 'MEH>  
A/Cross-references: GB:X03045; NID:928783; PIDN:CAA26850.1; PID:9929609  
R/Hospattanakar, A.V.; Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.B.  
Biochem. Biophys. Res. Commun. 148, 279-285, 1987  
A/Title: Identification of a novel in-frame translational stop codon in human intestine  
A/Reference number: A29659; MUID:88049670; PMID:2445342  
A/Accession: A29659  
A/Molecule type: mRNA  
A/Residues: 2169-2179, 'HOS>  
A/Note: the sequence shown represents the carboxyl end of apolipoprotein B-48  
ch encodes the 250K ap0B-48, CAA encoding 2180-Gln is substituted by the stop codon TAA,  
R/Yang, C.; Kim, T.W.; Weng, S.; Lee, B.; Yang, W.; Gotto Jr., A.M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 5523-5527, 1990  
A/Title: Isolation and characterization of bulbhydryl and disulfide peptides of human ap  
A/Reference number: A35783; MUID:90319144; PMID:2115173  
A/Accession: A35783  
A/Molecule type: Protein  
A/Residues: 28-41, 76-97, 'I', 99-100, 175-193, 206-215, 239-249, 259-266, 357-399, 455-490, 512-5

A>Note: cysteines at positions 112, 1422, 1505, 1662, 3761, 3917, and 4217 have free su  
 R:Laebouff, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J.  
 FEMS Lett. 170, 105-108, 1984  
 A>Title: Human apolipoprotein B: partial amino acid sequence.  
 C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
 C/Accession: JH0102  
 A:Reference number: A22006; MUID:84208786; PMID:6373369  
 A:Accession: A22006  
 A:Molecule type: protein  
 A:Residues: 873-892, 'K', 894-896 <LE1>  
 A:Accession: B22006  
 A:Molecule type: protein  
 A:Residues: 113, 'V', 315-3130, 'R', 3132-3133, 'P', 3135-3136, 'R' <LE2>  
 R:Blackhart, B.D.; Ludwig, E.M.; Piorotti, V.R.; Calafat, L.; Onasch, M.A.; Wallis, S.C.;  
 J. Biol. Chem. 261, 15364-15367, 1986  
 A>Title: Structure of the human apolipoprotein B gene.  
 A:Reference number: A92564; MUID:87057153; PMID:2946672  
 A:Contents: annotation; gene structure  
 R:Wenger, R.; Piltzner, R.; Stoffel, W.  
 Biol. Chem. Hoppe-Seyler 368, 419-425, 1987  
 A>Title: Studies on the organization of the human apolipoprotein B 100 gene.  
 A:Reference number: A90715; MUID:87271140; PMID:2886136  
 A:Contents: annotation; gene structure  
 R:Weisgraber, K.H.; Rall Jr., S.C.  
 J. Biol. Chem. 262, 11097-11103, 1987  
 A>Title: Human apolipoprotein B-100 heparin-binding sites.  
 A:Reference number: A92605; MUID:87280197; PMID:3301850  
 A:Contents: annotation; heparin binding and disulfide bond  
 R:Dacht, N.; Lee, D.M.; Mok, T.  
 Biochem. Biophys. Res. Commun. 137, 493-499, 1986  
 A>Title: Apolipoprotein B is a calcium binding protein.  
 A:Reference number: A90125; MUID:86242245; PMID:3087360  
 A:Contents: annotation; calcium binding  
 R:Carlsson, P.; Olofsson, S.O.; Bondjers, G.; Darnfors, C.; Wiklund, O.; Bjursell, G.  
 Nucleic Acids Res. 13, 8613-8626, 1985  
 A>Title: Molecular cloning of human apolipoprotein B cDNA.  
 A:Reference number: I37178; MUID:86093680; PMID:3841204  
 A:Accession: I37180

Query Match 100.0%; Score 54; DB 1; Length 4563;  
 Best Local Similarity 100.0%; Pred. No. 0.091;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTRLTRKRGK 11  
 |||||  
 Db 3384 TTRLTRKRGK 3394

## RESULT 3

C60950  
 A:apolipoprotein B-100 - golden hamster (fragment)  
 C/Species: Mesocricetus auratus (golden hamster)  
 C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C/Accession: C60950  
 R:Law, A.; Scott, J.  
 J. Lipid Res. 31, 1109-1120, 1990  
 A>Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL  
 A:Reference number: A60950; MUID:90324804; PMID:2373961  
 A:Accession: C60950  
 A:Molecule type: DNA  
 A:Residues: 1-269 <LAW>  
 A:Cross-references: UNIPROT:060537; UNIPROT:060536  
 C:Superfamily: apolipoprotein B  
 C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

Query Match 92.6%; Score 50; DB 2; Length 269;  
 Best Local Similarity 90.9%; Pred. No. 0.044;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTRLTRKRGK 11  
 |||||  
 Db 215 TTRLTRKRGK 225

## RESULT 4

JH0102  
 A:apolipoprotein B - golden hamster (fragment)  
 C/Species: Mesocricetus auratus (golden hamster)  
 C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
 C/Accession: JH0102  
 R:Smith, T.J.  
 submitted to GenBank, June 1990  
 A:Reference number: A38864  
 A:Accession: JH0102  
 A:Molecule type: DNA  
 A:Residues: 1-779 <SM1>  
 A:Cross-references: UNIPROT:060536; GB:M35187  
 A>Note: this is a revision to the sequence from reference JH0101  
 R:Smith, T.J.; Hautama, D.; Maeda, N.  
 Gene 87, 309-310, 1990  
 A>Title: Sequence of the putative low-density lipoprotein receptor-binding regions of ap  
 A:Reference number: JH0101; MUID:90236327; PMID:2332175  
 A:Contents: annotation  
 A>Note: this sequence has been revised in reference A38864  
 C:Genetics: apob  
 A:Gene: apob  
 C:Superfamily: apolipoprotein B  
 C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein,  
 F:435-445/Region: receptor binding  
 F:646-656/Region: receptor binding

Query Match 92.6%; Score 50; DB 2; Length 779;  
 Best Local Similarity 90.9%; Pred. No. 0.11;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTRLTRKRGK 11  
 |||||  
 Db 641 TTRLTRKRGK 651

## RESULT 5

A60950  
 A:apolipoprotein B-100 - rabbit (fragment)  
 C/Species: Oryctolagus cuniculus (domestic rabbit)  
 C/Date: 31-Dec-1993 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
 C/Accession: A60950  
 R:Law, A.; Scott, J.  
 J. Lipid Res. 31, 1109-1120, 1990  
 A>Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL  
 A:Reference number: A60950; MUID:90324804; PMID:2373961  
 A:Accession: A60950  
 A:Molecule type: mRNA  
 A:Residues: 1-274 <LAW>  
 A:Cross-references: UNIPROT:07M2U9  
 A>Note: authors translated the codon GAT for residue 155 as His  
 C:Superfamily: apolipoprotein B  
 C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein,

Query Match 81.5%; Score 44; DB 2; Length 274;  
 Best Local Similarity 81.8%; Pred. No. 0.66;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TTRLTRKRGK 11  
 |||||  
 Db 220 TTRLTRKRGK 230

## RESULT 6

E60950  
 A:apolipoprotein B-100 - chicken (fragment)  
 C/Species: Gallus gallus (chicken)  
 C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C/Accession: E60950  
 R:Law, A.; Scott, J.  
 J. Lipid Res. 31, 1109-1120, 1990  
 A>Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL  
 A:Reference number: A60950; MUID:90324804; PMID:2373961  
 A:Accession: E60950

A:Molecule type: mRNA  
 A:Residues: 1-275 <LAM>  
 A:Cross-references: UNIPROT:Q7L277  
 C:Superfamily: apolipoprotein B  
 C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

## Query Match

Best Local Similarity 81.5%; Score 44; DB 2; Length 275;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTRLTRKRGK 11  
 DB 220 TSTRKRGK 230

## RESULT 7

JH0101

C:Species: Mus musculus (house mouse)  
 C>Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text\_change 09-Jul-2004

R:Smith, T.J.; Hautamaa, D.; Maeda, N.  
 Gene 87, 309-310, 1990

A:Title: Sequence of the putative low-density lipoprotein receptor-binding regions of ap

A:Reference number: JH0101; MUID:90236327; PMID:2332175  
 A:Accession: JH0101  
 A:Molecule type: DNA

A:Residues: 1-784 <SMI>

A:Cross-references: UNIPROT:Q61314; GB:M5186  
 R:Smith, T.; Hautamaa, D.; Maeda, N.  
 submitted to the EMBL Data Library, May 1989

A:Reference number: S33128  
 A:Accession: S33128

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-531, 'S', 533-784 <SM2>

A:Cross-references: EMBL:X15191

R:Law, A.; Scott, J.

J. Lipid Res. 31, 1109-1120, 1990

A:Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL

A:Reference number: A60950; MUID:90324604; PMID:2373961

A:Accession: D60950

A:Molecule type: mRNA

A:Residues: 427-531, 'S', 533-700 <LAM>

C:Genetics:

A:Gene: MGI:Apob

A:Cross-references: MGI:88052

C:Superfamily: apolipoprotein B

C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

F:435-445/Region: receptor binding

F:646-656/Region: receptor binding

Query Match

Best Local Similarity 81.5%; Score 44; DB 2; Length 784;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTRLTRKRGK 11  
 DB 646 TSTRKRGK 656

## RESULT 8

AH0906

C:Species: Salmonella enterica subsp. enterica serovar Typhi  
 C>Date: 09-Nov-2001 #sequence revision 09-Nov-2001 #text\_change 18-Nov-2002

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, S.; Moule, S.; O'Geary, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov  
 A:Reference number: AH0906; MUID:21534947; PMID:11677608  
 A:Accession: AH0906  
 A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-309 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD07846.1; PID:G16504394; GSPDB:GN00176

C:Genetics:

A:Gene: STY3508

C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486

Query Match

Best Local Similarity 79.6%; Score 43; DB 2; Length 309;  
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTRLTRKRGK 11  
 DB 169 TTRLRERGLK 179

## RESULT 9

E65112

C:Species: Escherichia coli  
 C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M., cc

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: E65112

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-309 <BLAT>

A:Cross-references: UNIPROT:P45476; GB:AE000400; GB:U00096; NID:G2367203; PIDN:AACT624

A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: yncC

C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486

Query Match

Best Local Similarity 75.9%; Score 41; DB 1; Length 309;  
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTRLTRKRGK 11  
 DB 169 TTRLRERGLK 179

## RESULT 10

E83985

C:Species: Escherichia coli (strain O157:H7, substrain EDL9  
 C>Date: 16-Feb-2001 #sequence revision 16-Feb-2001 #text\_change 09-Jul-2004

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

Science 292, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: E83985

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-309 <STO>

A:Cross-references: UNIPROT:P45476; GB:AE005174; NID:G12517832; PIDN:AA658345.1; GSPDB:G

C:Genetics:

A:Gene: yncC

C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486

Query Match

Best Local Similarity 75.9%; Score 41; DB 2; Length 309;  
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11  
|:|:|:|:|:|  
Db 169 TTOLARQKGLK 179

## RESULT 11

B01140  
hypothetical protein EC64090 [imported] - Escherichia coli (strain O157:H7, substrain R1)  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C:Accession: B01140  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene A:Reference number: A59629; MUID:21156231; PMID:11258796  
A:Accession: B01140  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-309 <HAV>  
A:Cross-references: UNIPROT:P45476; GB:BA000007; PIDN:BA037513.1; PID:g13363563; GSPDB:C  
A:Experimental source: strain O157:H7, substrain R1MD 0509952  
C:Genetics:  
A:Gene: EC64090  
C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486

Query Match 75.9%; Score 41; DB 2; Length 309;  
Best Local Similarity 72.7%; Pred. No. 2.8;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11  
|:|:|:|:|:|  
Db 169 TTOLARQKGLK 179

## RESULT 12

BWABSE  
bimE protein - Emericella nidulans  
C:Species: Emericella nidulans, Aspergillus nidulans  
C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
C:Accession: A37879  
R:Engle, D.B.; Osman, S.A.; Osman, A.H.; Rosborough, S.; Xiang, X.; Morris, N.R. J. Biol. Chem. 265, 16132-16137, 1990  
A:Title: A negative regulator of mitosis in Aspergillus is a putative membrane-spanning A:Reference number: A37879; MUID:90375468; PMID:1697851  
A:Accession: A37879  
A:Molecule type: mRNA  
A:Residues: 1-2073 <ENG>  
A:Cross-references: UNIPROT:P24686; GB:M59705; GB:J05607; NID:g168026; PIDN:AAA51478.1; C:Note: In addition to three predicted transmembrane domains, there are several potential asen kinases, and one sequence that resembles a nuclear localization signal  
C:Comment: This protein is part of a regulatory pathway that includes the nimA protein K ter mitosis and prevent them from leaving mitosis.  
C:Genetics:  
A:Gene: bimE  
C:Superfamily: bimE protein  
C:Keywords: cell cycle control; mitosis; transmembrane protein  
F:1633-1643/Domain: transmembrane #status predicted <TM1>  
F:1685-1703/Domain: transmembrane #status predicted <TM2>  
F:1746-1764/Domain: transmembrane #status predicted <TM3>

Query Match 71.3%; Score 38.5; DB 1; Length 2073;  
Best Local Similarity 90.9%; Pred. No. 47;  
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 TTRLT-RKRG 10  
|:|:|:|:|:|  
Db 831 TTRLTRKRGK 841

## RESULT 13

## S65460

apolipoprotein B - Atlantic salmon (fragment)  
C:Species: Salmo salar (Atlantic salmon)  
C:Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: S65460; I51362  
R:Babin, P.J.; Deryckere, F.; Gannon, F. Eur. J. Biochem. 230, 45-51, 1995  
A:Title: Presence of an extended duplication in the putative low-density-lipoprotein rec A:Reference number: I51362; MUID:95324549; PMID:7541349  
A:Accession: S65460  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-1058 <BAB>  
A:Cross-references: UNIPROT:Q91480; EMBL:X81856; NID:98564619; PIDN:CAA57449.1; PID:g8546  
A:Experimental source: liver  
C:Genetics:  
A:Gene: apob  
C:Superfamily: apolipoprotein B  
C:Keywords: calcium; cholesterol metabolism; chylomicron; glycoprotein; intestine; LDL;

Query Match 70.4%; Score 38; DB 2; Length 1058;  
Best Local Similarity 72.7%; Pred. No. 32;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11  
|:|:|:|:|:|  
Db 501 TSSLTRKRGK 511

## RESULT 14

JT0382  
apolipoprotein B - pig (fragments)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: JT0382; I46567; I46568  
R:Maeda, N.; Ebert, D.L.; Doers, T.M.; Newman, M.; Hasler-Rapacz, J.; Attie, A.D.; Rapacz, Gene 70, 213-229, 1988  
A:Title: Molecular genetics of the apolipoprotein B gene in pigs in relation to atheros A:Reference number: JT0382; MUID:89108006; PMID:2905687  
A:Accession: JT0382  
A:Molecule type: DNA  
A:Residues: 1-1778 <MAE>  
A:Cross-references: UNIPROT:Q29020; UNIPROT:Q29433  
R:Maeda, N.; Ebert, D.L.; Doers, T.M.; Newman, M.; Hasler-Rapacz, J.O.; Attie, A.D.; Rap Gene 69, 213-229, 1988  
A:Title: Molecular genetics of the apolipoprotein B gene in pigs in relation to atheros A:Reference number: I46567  
A:Accession: I46567  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 239-1778 <MA2>  
A:Cross-references: GB:M2647; NID:g164367; PIDN:AAA30997.1; PID:g164370  
C:Comment: Apolipoprotein B is the predominant protein component of the low-density lipop C:Genetics:  
A:Gene: apob  
A:Introns: 39/3; 88/3; 159/2; 238/3; 1133/1; 1171/2; 1232/3  
A:Note: The list of introns may be incomplete  
C:Superfamily: apolipoprotein B  
C:Keywords: atherosclerosis; cholesterol metabolism; LDL; lipid binding; lipoprotein

Query Match 70.4%; Score 38; DB 2; Length 1778;  
Best Local Similarity 72.7%; Pred. No. 51;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11  
|:|:|:|:|:|  
Db 588 TSSLTRKRGK 598

RESULT 15

146569

apolipoprotein B - pig (fragment)

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004

C/Accession: 146569

R/Putrell, C.; Maeda, N.; Ebert, D.L.; Kaiser, M.; Lund-Katz, S.; Sturley, S.L.; Kodoyia

J. Lipid Res. 34, 1323-1335, 1993

A/Title: Nucleotide sequence encoding the carboxyl-terminal half of apolipoprotein B

A/Reference number: 146569; PMID:94014802; PMID:8409766

A/Accession: 146569

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-2629 <PUR>

A/Cross-references: UNIPROT:Q29021; GB:L11235; NID:G164371; PIDN:AAA74655.1; PID:G951375

C/Genetics:

A/Gene: APOB

C/Intons: 1984/1; 2022/2; 2083/3

C/Superfamily: apolipoprotein B

Query Match

Best Local Similarity 70.4%; Score 38; DB 2; Length 2629;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11

Db 1438 TSLMKRRGLK 1448

Search completed: January 12, 2005, 13:31:57

Job time : 21.2258 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 12, 2005, 12:49:11 ; Search time 109.645 Seconds  
(without alignments)  
57.724 Million cell updates/sec

Title: US-10-657-404A-2  
Perfect score: 54  
Sequence: 1 TTRLTRKRGK 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues  
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	414	2 QYOR5	QYOR5 aocus vocif
2	54	100.0	596	2 Q28473	Q28473 macaca fasc
3	54	100.0	3262	2 Q13788	Q13788 homo sapien
4	54	100.0	4563	1 APB_HUMAN	P04114 homo sapien
5	54	100.0	4563	2 Q2600	Q2600 homo sapien
6	50	92.6	421	2 Q7TN68	Q7TN68 glaucomye v
7	50	92.6	432	2 Q7YR10	Q7YR10 diceros bic
8	50	92.6	436	2 Q7YOM8	Q7YOM8 nyctimene a
9	50	92.6	438	2 Q7YOM7	Q7YOM7 pteropus hy
10	50	92.6	438	2 Q7YR04	Q7YR04 roussetus a
11	50	92.6	445	2 Q7YR08	Q7YR08 chaetophrac
12	50	92.6	445	2 Q7TN64	Q7TN64 agouti paca
13	50	92.6	445	2 Q7TN71	Q7TN71 hydrochoeru
14	50	92.6	445	2 Q7TN72	Q7TN72 etethizonu d
15	50	92.6	780	2 Q60536	Q60536 mesocricetu
16	50	92.6	780	2 Q60537	Q60537 mesocricetu
17	48	88.9	387	2 Q7YON2	Q7YON2 phalangor o
18	48	88.9	445	2 Q7TN70	Q7TN70 dinomys bra
19	47	87.0	407	2 Q7TN65	Q7TN65 athemus a
20	47	87.0	412	2 Q7TN69	Q7TN69 hystrix bra
21	44	81.5	274	2 Q7M2U9	Q7M2U9 oryctolagus
22	44	81.5	275	2 Q7L277	Q7L277 gallus galli
23	44	81.5	304	2 Q7YOP9	Q7YOP9 echinops te
24	44	81.5	314	2 Q7YON8	Q7YON8 ictonyx scr
25	44	81.5	316	2 Q7YOP3	Q7YOP3 nandania bi
26	44	81.5	318	2 Q7YON9	Q7YON9 zalophus ca
27	44	81.5	319	2 Q7YOP0	Q7YOP0 vulpes vulp
28	44	81.5	319	2 Q7YOP2	Q7YOP2 panthera le
29	44	81.5	320	2 Q7YOP4	Q7YOP4 panis sp. k
30	44	81.5	361	2 Q7YOP8	Q7YOP8 amblyomus
31	44	81.5	386	2 Q7YOR1	Q7YOR1 tupia tana

32	44	81.5	392	2 Q7YR11	Q7YR11 tarsius syr
33	44	81.5	411	2 Q7YOP7	Q7YOP7 ochotona pr
34	44	81.5	422	2 Q7YR12	Q7YR12 talpa europ
35	44	81.5	423	2 Q7YQ09	Q7YQ09 sorex monti
36	44	81.5	426	2 Q7YOR2	Q7YOR2 alces alces
37	44	81.5	429	2 Q7YQ08	Q7YQ08 crocidura f
38	44	81.5	438	2 Q7YOR4	Q7YOR4 balaena myx
39	44	81.5	441	2 Q7YOR3	Q7YOR3 phocaenoid
40	44	81.5	443	2 Q7YON5	Q7YON5 megaderma l
41	44	81.5	443	2 Q7YOP6	Q7YOP6 lepus ameri
42	44	81.5	445	2 Q7YON6	Q7YON6 bradydus tr
43	44	81.5	445	2 Q7YQ07	Q7YQ07 capinus bai
44	44	81.5	445	2 Q7YOR0	Q7YOR0 cynocephal
45	44	81.5	445	2 Q7YR07	Q7YR07 lemur catca

## ALIGNMENTS

RESULT 1  
QYOR5 PRELIMINARY; PRT; 414 AA.  
AC QYOR5;  
DT 01-OCT-2003 (TREMBlrel. 25, Created)  
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Apolipoprotein B 100 (Fragment).  
GN Name=apob-100;  
OS Aotus vociferans (Spix's owl monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.  
OX NCBI\_Taxid=57176;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22761261; PubMed=12878460;  
RA Amline-Madsen H., Koefli K.-P., Wayne R.K., Springer M.S.;  
RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
evidence for eutherian relationships";  
RL Mol. Phylogenet. Evol. 28:225-240(2003).  
DR EMBL; AF548396; AAP97352.1; -.  
KW Lipoprotein.  
FT NON\_TER 1 1  
FT SEQUENCE 414 AA; 45955 MW; EEP8492157E1BDE CRC64;  
SQ  
Query Match 100.0%; Score 54; DB 2; Length 414;  
Best Local Similarity 100.0%; Pred. No. 0.033;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTRLTRKRGK 11  
DB 257 TTRLTRKRGK 267  
RESULT 2  
Q28473 PRELIMINARY; PRT; 596 AA.  
ID Q28473;  
AC Q28473;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Apolipoprotein B (Fragment).  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Macaca.  
OX NCBI\_Taxid=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Liver;  
RC MEDLINE=92075708; PubMed=1742325;  
RA Pape M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,  
Marotit K.R., Melchior G.W.;

RT "Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional regulation."  
 RL Biochim. Biophys. Acta 1086:326-334 (1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Murray R.;  
 RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X15737; CAA33755.1; -.  
 DE PIR; S32802; S32802.  
 KW Lipoprotein.  
 FT NON TER  
 SQ SEQUENCE 596 AA; 66757 MW; B13BA74E25C3120 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 596;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TTRLTTRKRGK 11  
 Db 225 TTRLTTRKRGK 235

RESULT 3  
 ID 013788 PRELIMINARY; PRT; 3262 AA.  
 AC 013788;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DE AP0B protein (Fragment).  
 GN Name=AP0B;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carlsson P., Darntors C., Olofsson S.O., Bjureell G.;  
 RT "Analysis of the human apolipoprotein B gene; complete structure of the B-74 region."  
 RL Gene 49:29-51 (1986).  
 DR EMBL; M15421; AAA51758.1; -.  
 DR PIR; A27850; LPHDB.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0005319; F:lipid transporter activity; NAS.  
 FT NON TER 1  
 SQ SEQUENCE 3262 AA; 370140 MW; 56603BC0618DD40D CRC64;

Query Match 100.0%; Score 54; DB 2; Length 3262;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TTRLTTRKRGK 11  
 Db 2083 TTRLTTRKRGK 2093

RESULT 4  
 ID APB\_HUMAN STANDARD; PRT; 4563 AA.  
 AC P04114; 000502; 013787;  
 DT 01-NOV-1986 (Rel. 03, Created)  
 DT 05-JUL-2004 (Rel. 03, Last sequence update)  
 DE Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein B-48 (Apo B-48)].  
 GN Name=AP0B;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,  
 RA Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;  
 RT "Complete cDNA and derived protein sequence of human apolipoprotein B-100."  
 RL Nucleic Acids Res. 14:7501-7503 (1986).  
 RP SEQUENCE FROM N.A., AND VARIANT GLU-4181.  
 RA Knott T.C., Blackhart B.D., Pierotti V.R., Caiati L., Fortier C.,  
 RT "DNA sequence of the human apolipoprotein B gene."  
 RL DNA 6:363-372 (1987).  
 RP SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.  
 RA Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,  
 RA Goto A.M., Jr., Chan L.;  
 RT "The complete cDNA and amino acid sequence of human apolipoprotein B-100."  
 RL J. Biol. Chem. 261:12918-12921 (1986).  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=87041416; PubMed=3464946;  
 RA Lee S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,  
 RA Lee N., Brewer H.B., Jr.;  
 RT "Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino acid sequence."  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146 (1986).  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=87161758; PubMed=3030729;  
 RA Ciadara C., Hadzopoulou-Ciadara M., Nolte R.T., Atkinson D.,  
 RA Zannis V.I.;  
 RT "The complete sequence and structural analysis of human apolipoprotein B-100: relationship between ap0B-100 and ap0B-48 forms."  
 RL EMBO J. 5:13495-13507 (1986).  
 RP SEQUENCE OF 709-906 FROM N.A.  
 RA MEDLINE=85270450; PubMed=3860836;  
 RA Deeb S.S., Motulsky A.G., Albers J.J.;  
 RT "A partial cDNA clone for human apolipoprotein B."  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986 (1985).  
 RP SEQUENCE OF 3056-3159 FROM N.A.  
 RA MEDLINE=86041888; PubMed=3903560;  
 RA Kirschgesner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz B., Lusis A.J.;  
 RT "Human apolipoprotein B: identification of cDNA clones and characterization of mRNA."  
 RL Nucleic Acids Res. 13:6937-6953 (1985).  
 RP SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A., AND VARIANT GLU-4181.  
 RA Carlsson P., Olofsson S.O., Bondjers G., Darntors C., Wiklund O.,  
 RA Bjursell G.;  
 RT "Molecular cloning of human apolipoprotein B cDNA."  
 RL Nucleic Acids Res. 13:6813-6826 (1985).  
 RP SEQUENCE OF 3109-4563 FROM N.A.  
 RA MEDLINE=85300528; PubMed=2994225;  
 RA Knott T.J., Rall S.C., Jr., Innerarity T.L., Jacobson S.F., Urdea M.S.,  
 RA Levy-Wilson B., Powell L.M., Pease R.J., Bddy R., Nakai H., Byers M.,  
 RA Priestley L.M., Robertson E., Rall L.B., Betsholtz C., Shows T.B.,  
 RA Mahley R.W., Scott J.;  
 RT "Human apolipoprotein B: structure of carboxyl-terminal domains, sites of gene expression, and chromosomal localization."  
 RL Science 230:37-43 (1985).  
 RN [10]

RP SEQUENCE OF 1-291 FROM N.A.  
 RX MEDLINE=86149325; PubMed=351317;  
 RA Procter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,  
 RA Chen G.C., Kirschner S.W., McEnroe G., Kane J.P.;  
 RT "Isolation of a cDNA clone encoding the amino-terminal region of human  
 RT apolipoprotein B.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986).  
 [11]  
 RP SEQUENCE OF 1-1670 FROM N.A., AND VARIANT IIE-98.  
 RX MEDLINE=86287319; PubMed=3461454;  
 RA Procter A.A., Hardman D.A., Sato K.Y., Schilling J.W., Yamanaka M.,  
 RA Hori Y.J., Hjerrild K.A., Chen G.C., Kane J.P.;  
 RT "Analysis of cDNA clones encoding the entire B-26 region of human  
 RT apolipoprotein B.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986).  
 [12]  
 RP PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-B48.  
 RX MEDLINE=86018019; PubMed=3559919;  
 RA Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,  
 RA Silbermann S.R., Cai S.-J., Deslypere J.P., Roseneau M.,  
 RA Gotto A.M. Jr., Li W.-H., Chan L.;  
 RT "Apolipoprotein B-48 is the product of a messenger RNA with an organ-  
 RT specific in-frame stop codon.";  
 RL Science 238:363-366(1987).  
 [13]  
 RP DOMAIN.  
 RX MEDLINE=87039351; PubMed=3773997;  
 RA Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,  
 RA Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,  
 RA Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,  
 RA Levy-Wilson B., Scott J.;  
 RT "Complete protein sequence and identification of structural domains of  
 RT human apolipoprotein B.";  
 RL Nature 323:734-738(1986).  
 [14]  
 RP DOMAIN.  
 RX MEDLINE=87039351; PubMed=3773997;  
 RA Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T.,  
 RA Tanikura M., Li W.-H., Sparrow D.A., Deloof H., Roseneau M.,  
 RA Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L.;  
 RT "Sequence, structure, receptor-binding domains and internal repeats of  
 RT human apolipoprotein B-100.";  
 RL Nature 323:738-742(1986).  
 [15]  
 RP CALCIUM-BINDING DATA.  
 RX MEDLINE=86242245; PubMed=3087360;  
 RA Dashti N., Lee D.M., Mok T.;  
 RT "Apolipoprotein B is a calcium binding protein.";  
 RL Biochem. Biophys. Res. Commun. 137:493-499(1986).  
 [16]  
 RP PALMITOYLATION OF CYS-1112.  
 RX MEDLINE=20143590; PubMed=10679026;  
 RA Zhao Y., McCabe J.B., Vance J., Berthiaume L.G.;  
 RT "Palmitoylation of apolipoprotein B is required for proper  
 RT intracellular sorting and transport of cholesterol esters and  
 RT triglycerides.";  
 RL Mol. Biol. Cell 11:721-734(2000).  
 [17]  
 RP VARIANT SER-4338.  
 RX MEDLINE=91071750; PubMed=1979313;  
 RA Navajas M., Laurent A.-M., Morel J.-F., Ragab A., Cambou J.-P.,  
 RA Cuny G., Cambien F., Roizes G.;  
 RT "Detection by denaturing gradient gel electrophoresis of a new  
 RT polymorphism in the apolipoprotein B gene.";  
 RL Hum. Genet. 86:91-93(1990).  
 [18]  
 RP VARIANT FDB GLN-1527.  
 RX MEDLINE=89098975; PubMed=2563166;  
 RA Sorta L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,  
 RA McCarthy B.J.;  
 RT "Association between a specific apolipoprotein B mutation and familial  
 RT defective apolipoprotein B-100.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).  
 [19]

RP VARIANT LEU-2739.  
 RX MEDLINE=91016874; PubMed=2216805;  
 RA Huang L.-S., Gavish D., Breslow J.L.;  
 RT "Sequence polymorphism in the human apob gene at position 8344.";  
 RL Nucleic Acids Res. 18:5922-5922(1990).  
 [20]  
 RP VARIANT FDB CYS-3558.  
 RX MEDLINE=95190020; PubMed=7083971;  
 RA Pullinger C.R., Hennessey L.K., Chatterton J.E., Liu W., Love J.A.,  
 RA Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.;  
 RT "Familial ligand-defective apolipoprotein B. Identification of a new  
 RT mutation that decreases LDL receptor binding affinity.";  
 RL J. Clin. Invest. 95:1225-1234(1995).  
 [21]  
 RP VARIANTS LEU-1437, SER-1914, LYS-2566, THR-3121, ALA-3945, MET-4128  
 RP AND THR-4481.  
 RX MEDLINE=97044521; PubMed=8889592;  
 RA Poirier O., Ricard S., Behague I., Souriau C., Evans A.E.,  
 RA Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;  
 RT "Detection of new variants in the apolipoprotein B (Apo B) gene by  
 RT PCR-SSCP.";  
 RL Hum. Mutat. 8:282-285(1996).  
 [22]  
 RP VARIANTS FDB GLN-3527 AND CYS-3558.  
 RX MEDLINE=97403938; PubMed=9259199;  
 RA Rabes J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G.,  
 RA Krempf M., Giraudet P., Junien C., Boileau C.;  
 RT "Familial ligand-defective apolipoprotein B-100: simultaneous  
 RT detection of the ARG3500->GLN and ARG3531->CYS mutations in a French  
 RT population.";  
 RL Hum. Mutat. 10:160-163(1997).  
 [23]  
 RP VARIANTS SER-1914, ARG-1923, LEU-2739, ASP-3319, THR-3427, GLN-3432  
 RP AND ILE-3921.  
 RX MEDLINE=98141125; PubMed=9490296;  
 RA Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;  
 RT "Screening for mutations of the apolipoprotein B gene causing  
 RT hypocholesterolemia.";  
 RL Hum. Genet. 102:44-49(1998).  
 CC -I- FUNCTION: Apolipoprotein B is a major protein constituent of  
 CC chylomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apo  
 CC B-100 functions as a recognition signal for the cellular binding  
 CC and internalization of LDL particles by the apoB/E receptor.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 Query Match 100.0%; Score 54; DB 1; Length 4563;  
 Best Local Similarity 100.0%; Pred. No. 0.42;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTRLTRKRGK 11  
 DB 3384 TTRLTRKRGK 3394  
 RESULT 5  
 ID Q72600 PRELIMINARY; PRT; 4563 AA.  
 AC Q72600;  
 DT 01-OCT-2003 (TREMBlrel. 25, Created)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Apolipoprotein B (Including Ag(X) antigen).  
 GN Name=APOB;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,  
 RA Ahearn M.O., Kuidanek S.A., Rajkumar N., Toch E.J., Yi Q.,  
 RA Nickerson D.A.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY24608; AAF72970.1; -.  
 DR GO: GO:0005319; F:lipid transporter activity; IEA.  
 DR GO: GO:0006669; P:lipid transport; IEA.  
 DR InterPro: IPR009454; DUF1081.  
 DR InterPro: IPR001747; Lipid\_transprt\_N.  
 DR Pfam: PF06448; DUF1081; 1-  
 DR Pfam: PF01347; Vitellinogenin\_N; 1.  
 DR SMART: SM00638; LPD\_N; 1.  
 KW Lipoprotein.  
 SQ SEQUENCE 4563 AA; 515553 MW; 030B34167CEDC63C CRC64;

Query Match 100.0%; Score 54; DB 2; Length 4563;  
 Best Local Similarity 100.0%; Pred. No. 0.42;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTRLTRKRGK 11  
 DB 3384 TTRLTRKRGK 3394

RESULT 6  
 O7TN68 PRELIMINARY; PRT; 421 AA.  
 AC O7TN68:  
 DT 01-OCT-2003 (TREMBlrel. 25; Created)  
 DT 01-OCT-2003 (TREMBlrel. 25; Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25; Last annotation update)  
 DE Apolipoprotein B (Fragment).  
 OS Glaucomys volans (Southern flying squirrel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Petauristinae;  
 OC Glaucomys;  
 OC NCBI\_Taxid=64683;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22761261; PubMed=12878460;  
 RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;  
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
 RT evidence for eutherian relationships.";  
 RL Mol. Phylogenet. Evol. 28:225-240(2003).  
 DR EMBL: AY243379; AAP50767.1; -.  
 KW Lipoprotein.  
 FT NON TER 1  
 FT NON TER 421  
 SQ SEQUENCE 421 AA; 46747 MW; D47B7BD4F864FD1 CRC64;

Query Match 92.6%; Score 50; DB 2; Length 421;  
 Best Local Similarity 90.9%; Pred. No. 0.22;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTRLTRKRGK 11  
 DB 263 TTRLTRKRGK 273

RESULT 7  
 O7YR10 PRELIMINARY; PRT; 432 AA.  
 AC O7YR10:  
 DT 01-OCT-2003 (TREMBlrel. 25; Created)  
 DT 01-OCT-2003 (TREMBlrel. 25; Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25; Last annotation update)  
 DE Apolipoprotein B (Fragment).  
 OS Dicerus bicornis (Black rhinoceros).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Dicerus.  
 OC NCBI\_Taxid=9805;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22761261; PubMed=12878460;  
 RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;  
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
 RT evidence for eutherian relationships.";

RL Mol. Phylogenet. Evol. 28:225-240(2003).  
 DR EMBL: AY243375; AAP50763.1; -.  
 KW Lipoprotein.  
 FT NON TER 1  
 FT NON TER 432  
 SQ SEQUENCE 432 AA; 48171 MW; F27B7AB3604732C CRC64;

Query Match 92.6%; Score 50; DB 2; Length 432;  
 Best Local Similarity 90.9%; Pred. No. 0.22;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTRLTRKRGK 11  
 DB 274 TTRLTRKRGK 284

RESULT 8  
 O7YOM8 PRELIMINARY; PRT; 436 AA.  
 AC O7YOM8:  
 DT 01-OCT-2003 (TREMBlrel. 25; Created)  
 DT 01-OCT-2003 (TREMBlrel. 25; Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25; Last annotation update)  
 DE Apolipoprotein B 100 (Fragment).  
 GN Name=apob-100;  
 OS Nyctimene albigenter (Common tube-nosed fruit bat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;  
 OC Pteropodidae; Nyctimene.  
 OC NCBI\_Taxid=46988;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22761261; PubMed=12878460;  
 RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;  
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
 RT evidence for eutherian relationships.";  
 RL Mol. Phylogenet. Evol. 28:225-240(2003).  
 DR EMBL: AF548435; AAP97391.1; -.  
 KW Lipoprotein.  
 FT NON TER 1  
 FT NON TER 436  
 SQ SEQUENCE 436 AA; 48717 MW; 1CA47EAD72D2C629 CRC64;

Query Match 92.6%; Score 50; DB 2; Length 436;  
 Best Local Similarity 90.9%; Pred. No. 0.23;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTRLTRKRGK 11  
 DB 278 TTRLTRKRGK 288

RESULT 9  
 O7YOM7 PRELIMINARY; PRT; 438 AA.  
 AC O7YOM7:  
 DT 01-OCT-2003 (TREMBlrel. 25; Created)  
 DT 01-OCT-2003 (TREMBlrel. 25; Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25; Last annotation update)  
 DE Apolipoprotein B 100 (Fragment).  
 GN Name=apob-100;  
 OS Pteropus hypomelanus (Small flying fox).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;  
 OC Pteropodidae; Pteropus.  
 OC NCBI\_Taxid=9405;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22761261; PubMed=12878460;  
 RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;  
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
 RT evidence for eutherian relationships.";  
 RL Mol. Phylogenet. Evol. 28:225-240(2003).

DR EMBL: AF548436; AAP97392.1; -  
KW Lipoprotein.  
FT NON\_TER 1  
SQ SEQUENCE 438 AA; 48734 MW; 2BD5BCBF4E2CC41 CRC64;  
Query Match  
Best Local Similarity 92.6%; Score 50; DB 2; Length 438;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTRLTRKXGK 11  
Db 280 TSLRTRKXGK 290  
RESULT 10  
ID QYR04 PRELIMINARY; PRT; 438 AA.  
AC QYR04; 01-OCT-2003 (TREMBlrel. 25, Created)  
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
DE Apolipoprotein B (Fragment).  
OS Roussetus ampelicaudatus (Common roussette).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;  
OC Pteropodidae; Roussetus.  
OX NCBI\_TaxID=58083;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22761261; PubMed=12878460;  
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;  
RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
evidence for eutherian relationships.";  
RL Mol. Phylogenet. Evol. 28:225-240(2003).  
DR EMBL: AY243383; AAP50771.1; -  
KW Lipoprotein.  
FT NON\_TER 1  
FT NON\_TER 438  
SQ SEQUENCE 438 AA; 48597 MW; 41C890DEAF95C872 CRC64;  
Query Match  
Best Local Similarity 92.6%; Score 50; DB 2; Length 438;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTRLTRKXGK 11  
Db 280 TSLRTRKXGK 290  
RESULT 11  
ID QYR08 PRELIMINARY; PRT; 445 AA.  
AC QYR08; 01-OCT-2003 (TREMBlrel. 25, Created)  
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
DE Apolipoprotein B (Fragment).  
OS Chaetopharactes villosus (South American armadillo).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Edentata; Dasypodidae; Chaetopharactes.  
OX NCBI\_TaxID=29080;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22761261; PubMed=12878460;  
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;  
RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
evidence for eutherian relationships.";  
RL Mol. Phylogenet. Evol. 28:225-240(2003).  
DR EMBL: AY243378; AAP50766.1; -  
KW Lipoprotein.  
FT NON\_TER 1  
FT NON\_TER 445  
SQ SEQUENCE 445 AA; 445

SQ SEQUENCE 445 AA; 49564 MW; 2DA5DC3ED2F0FDD2 CRC64;  
Query Match  
Best Local Similarity 92.6%; Score 50; DB 2; Length 445;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTRLTRKXGK 11  
Db 287 TSLRTRKXGK 297  
RESULT 12  
ID QYTN64 PRELIMINARY; PRT; 445 AA.  
AC QYTN64; 01-OCT-2003 (TREMBlrel. 25, Created)  
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
DE Apolipoprotein B 100 (Fragment).  
GN Name=apob-100;  
OS Agouti paca (paca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognath; Agoutidae; Agouti.  
OX NCBI\_TaxID=108852;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22761261; PubMed=12878460;  
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;  
RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
evidence for eutherian relationships.";  
RL Mol. Phylogenet. Evol. 28:225-240(2003).  
DR EMBL: AF548417; AAP97373.1; -  
KW Lipoprotein.  
FT NON\_TER 1  
FT NON\_TER 445  
SQ SEQUENCE 445 AA; 49721 MW; 34AF7ABE90F121EF CRC64;  
Query Match  
Best Local Similarity 92.6%; Score 50; DB 2; Length 445;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTRLTRKXGK 11  
Db 287 TSLRTRKXGK 297  
RESULT 13  
ID QYTN71 PRELIMINARY; PRT; 445 AA.  
AC QYTN71; 01-OCT-2003 (TREMBlrel. 25, Created)  
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
DE Apolipoprotein B (Fragment).  
OS Hydrochoerus hydrochaeris (Capybara) (Carpincho).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognath; Hydrochaeridae;  
OC Hydrochaeris.  
OX NCBI\_TaxID=10149;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22761261; PubMed=12878460;  
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;  
RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
evidence for eutherian relationships.";  
RL Mol. Phylogenet. Evol. 28:225-240(2003).  
DR EMBL: AY243369; AAP50757.1; -  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; UNKNOWN\_1.  
KW Lipoprotein.  
FT NON\_TER 1  
FT NON\_TER 445  
SQ SEQUENCE 445 AA; 49520 MW; CBBA2DD53D7A18D2 CRC64;

Query Match 92.6%; Score 50; DB 2; Length 445;  
 Best Local Similarity 90.9%; Pred. No. 0.23;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTRLTRKRGK 11  
 |:|||||  
 DB 287 TSRLTRKRGK 297

Query Match 92.6%; Score 50; DB 2; Length 780;  
 Best Local Similarity 90.9%; Pred. No. 0.42;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTRLTRKRGK 11  
 |:|||||  
 DB 641 TSRLTRKRGK 651

Search completed: January 12, 2005, 13:30:54  
 Job time : 110.645 secs

RESULT 14  
 Q7TN72 PRELIMINARY; PRT; 445 AA.  
 ID Q7TN72  
 AC Q7TN72;  
 DT 01-OCT-2003 (TREMBlrel. 25, Created)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
 DE Apolipoprotein B (Fragment).  
 OS Erethizon dorsatum (North American porcupine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Erethizontidae;  
 OC Erethizon.  
 OX NCBI\_TaxID=34844;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=22761261; PubMed=12878460;  
 RX Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;  
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
 evidence for eutherian relationships.";  
 RL Mcl. Phylogenet. Evol. 28:225-240(2003).  
 DR EMBL; AF243368; AAF50756.1; -.  
 KW Lipoprotein.  
 FT NON\_TER 1 1  
 FT NON\_TER 445 445  
 SQ SEQUENCE 445 AA; 49617 MW; 9572FE5FE7625F2 CRC64;

Query Match 92.6%; Score 50; DB 2; Length 445;  
 Best Local Similarity 90.9%; Pred. No. 0.23;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTRLTRKRGK 11  
 |:|||||  
 DB 287 TSRLTRKRGK 297

RESULT 15  
 Q60536 PRELIMINARY; PRT; 780 AA.  
 ID Q60536  
 AC Q60536;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Hamster apolipoprotein (apob) (Fragment).  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=90236327; PubMed=2332175;  
 RX Smith T.J., Hautama D., Maeda N.;  
 RT "Sequence of the putative low-density lipoprotein receptor-binding  
 regions of apolipoprotein B in mouse and hamster.";  
 RL Gene 87:309-310(1990).  
 DR EMBL; M35187; AAA37059.1; -.  
 DR PIR; C60950; C60950.  
 DR PIR; JH0102; JH0102.  
 KW Lipoprotein.  
 FT NON\_TER 1 1  
 FT NON\_TER 780 780  
 SQ SEQUENCE 780 AA; 86625 MW; E371D1B2079D8F7E CRC64;



CC receptor-competent LDL particles do not require the complete apo B  
 CC sequence, which is large and tends to aggregate, to provide binding  
 CC affinity to an apo B protein receptor  
 XX  
 SO Sequence 11 AA;

Query Match 100.0%; Score 44; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 RLTRKRGK 9  
 |||||  
 3 RLTRKRGK 11  
 Db

RESULT 2  
 AAW57206  
 ID AAW57206 standard; peptide; 11 AA.  
 AC AAW57206;  
 XX  
 AC AAW57206;  
 XX  
 DT 03-AUG-1998 (first entry)  
 XX  
 DE Apo B 100 binding site peptide analogue peptide A.  
 XX  
 KW Apo B; binding site; receptor; cancer; drug delivery; anticancer;  
 KW growth supplement; non-natural lipid particle; low density lipoprotein;  
 KW LDL; receptor component; apo B100 receptor site.  
 XX  
 OS Synthetic.  
 XX

XX Key Location/Qualifiers  
 FH Modified-site 1 /note="attached to retinoic acid"  
 FT Modified-site 11 /note="attached to cholesterol"  
 FT  
 XX  
 PN W09813385-A2.  
 XX  
 PD 02-APR-1998.  
 XX  
 PF 25-SEP-1997; 97WO-GB002610.  
 XX  
 PR 27-SEP-1996; 96GB-00020153.  
 XX  
 PA (UYST ) UNIV STRATHCLYDE.  
 XX

PI Halbert GW, Owens MD, Baillie G;  
 XX  
 DR WPI; 1998-230637/20.  
 XX  
 XX

PT Non-natural lipid particle comprising peptide binding to apo B protein  
 PT receptor - useful as, e.g. vector for delivering drugs to cancer cells  
 PT that express this receptor.  
 XX

PS Claim 13; Fig 7; 73pp; English.

CC The present sequence represents a specifically claimed Apo B 100 binding  
 CC site peptide analogue which can be used as a component of a non-  
 CC naturally occurring, receptor-competent low density lipoprotein (LDL)  
 CC particle of the present invention. The LDL particle comprises at least 1  
 CC peptide component that has at least 1 binding site for an apo B protein  
 CC receptor and at least 1 lipophilic substituent. Also described in the  
 CC invention are peptides containing an apo B binding sequence with at least  
 CC 70% identity with sequences: KAEKKKKHH (1) or TTRRLTRKRGK (2), or their  
 CC dimers. Non-naturally occurring, receptor-competent LDL particles are  
 CC useful as: (i) drug-targeting vectors for delivering anticancer drugs to  
 CC cancer cells that express an apo B protein receptor, and (ii) additives  
 CC for cell culture media especially as growth supplements. Non-naturally  
 CC occurring, receptor-competent LDL particles do not require the complete  
 CC apo B sequence, which is large and tends to aggregate, to provide binding  
 CC affinity to an apo B protein receptor  
 XX

SO Sequence 11 AA;

Query Match 100.0%; Score 44; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 RLTRKRGK 9  
 |||||  
 2 RLTRKRGK 10  
 Db

RESULT 3  
 AAW87717  
 ID AAW87717 standard; peptide; 11 AA.  
 XX  
 AC AAW87717;  
 XX  
 DT 09-MAR-1999 (first entry)  
 XX  
 DE Analogue of residues 3359-3369 of apoprotein B 100.  
 XX  
 KW Analogue; apoprotein B 100; malondialdehyde; MDA; atherosclerosis;  
 KW apoprotein B-based low density lipoprotein; LDL; foam cell;  
 XX high affinity LDL receptor; cholesterol; epitope.  
 XX  
 OS Homo sapiens.  
 XX

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Modified-site 5 /note="conjugated to malondialdehyde (MDA)"  
 FT  
 FT  
 XX  
 PN W09842751-A1.  
 XX  
 PD 01-OCT-1998.  
 XX  
 PF 20-MAR-1998; 98WO-GB000677.  
 XX  
 PR 20-MAR-1997; 97GB-00005831.  
 XX  
 PA (UYLE-) UNIV LEICESTER.  
 XX

PI Lunec J, Bevan R, Griffiths H;  
 XX  
 DR WPI; 1999-045137/04.  
 XX  
 XX

PT Oxidised fragments of apoprotein B-based low density lipoprotein, LDL -  
 PT which inhibits LDL uptake by high affinity LDL receptor, useful e.g. in  
 PT treatment and diagnosis of atherosclerosis.  
 XX

PS Claim 2; Page 2; 23pp; English.

CC The present sequence is an analogue of apoprotein B 100. The peptide,  
 CC which has lys8 conjugated with malondialdehyde (MDA) inhibits uptake of  
 CC apoprotein B-based low density lipoprotein (LDL) (or partly modified  
 CC forms of LDL) by the high affinity LDL receptor. The peptide and its  
 CC analogues are useful in treatment and diagnosis, especially for  
 CC atherosclerosis. Atherosclerosis is characterised by thickening and  
 CC streaks containing foam cells and, secondly, the formation of fibrous  
 CC plaques within the artery. Foam cells are formed by endocytosis of  
 CC oxidised LDL by macrophages via a scavenger receptor, which causes cells  
 CC to take up more cholesterol than necessary via the high affinity LDL  
 CC receptors. The peptides of the invention are oxidised and present  
 CC epitopes which prevent oxidised LDL from being taken up by the scavenger  
 CC receptor, so preventing LDL uptake by the high affinity LDL receptor, and  
 CC possibly preventing foam cell formation  
 XX

SO Sequence 11 AA;

Query Match 100.0%; Score 44; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLTRKRGGLK 9  
| | | | |  
DB 1 RLTRKRGGLK 9

RESULT 4  
AAE21732  
ID AAE21732 standard; peptide; 11 AA.  
XX  
AC AAE21732;  
XX  
DT 16-JUL-2002 (first entry)  
XX  
DE BSMR effector peptide #2.  
XX  
KW Bone strength and mineralisation regulatory protein; BSMR; bone strength;  
KW mineralisation; ophthalmological; antidiabetic;  
KW bone density regulating transmembrane receptor; prosthetic device;  
KW surgical implant; diabetic retinopathy; hypertensive retinopathy;  
KW therapy; osteoporosis; prematurity; ocular vessel; eye disorder;  
KW osteopathic.  
XX  
OS Unidentified.  
XX  
PN WO200216553-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-US041788.  
XX  
PR 18-AUG-2000; 2000US-0226119P.  
PR 22-SEP-2000; 2000US-0234337P.  
PR 13-JUL-2001; 2001US-0304851P.  
XX  
XX (AVENTIS PHARMA SA.  
PA (HARD) HARVARD COLLEGE.  
PA (UYCA-) UNIV CASE WESTERN RESERVE.  
XX  
PI Warman ML, Gong Y, Olsen BR, Rawadi G, Roman-Roman S;  
XX  
XX WPI; 2002-323694/36.  
XX  
DR  
XX  
PT Polynucleotide encoding bone strength and mineralization regulatory  
XX  
XX protein useful for diagnosis or therapy of osteoporosis.  
XX  
PS Claim 9; Page 78; 124pp; English.  
XX  
CC The invention relates to bone strength and mineralisation regulatory  
CC protein (BSMR) and its corresponding nucleic acid sequence. BSMR DNA is  
CC useful for the diagnosis or therapy of osteoporosis and for regulating  
CC (increasing) bone strength and mineralisation in a human subject by  
CC activating a bone density regulating transmembrane receptor (BSMR  
CC protein). An expression vector comprising a promoter that is operably  
CC linked to BSMR DNA is useful for modulating bone density and for  
CC enhancing bone strength and mineralisation in a mammal cell. Composition  
CC comprising a BSMR effector is useful for treating osteoporosis and is  
CC useful particularly as a coating for prosthetic devices and surgical  
CC implants. BSMR is useful for screening lead pharmaceutical agents as BSMR  
CC effectors, which may be used to treat a range of eye disorders such as  
CC diabetic retinopathy, hypertensive retinopathy and retinopathy of  
CC prematurity, in which normal vascular growth and integrity of ocular  
CC vessels is disrupted. The present sequence is BSMR effector peptide  
XX  
SQ Sequence 11 AA;

Query Match 100.0%; Score 44; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.089;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLTRKRGGLK 9  
| | | | |  
DB 1 RLTRKRGGLK 9

RESULT 5  
ABU07938  
ID ABU07938 standard; peptide; 11 AA.  
XX  
AC ABU07938;  
XX  
DT 23-MAY-2003 (first entry)  
XX  
DE Apoprotein B 100, residues 3359-3369.  
XX  
KW Apoprotein B 100; Apo B; human; high affinity low density lipoprotein;  
KW LDL; LDL receptor; immunogen; atherosclerosis; foam cell formation.  
XX  
OS Homo sapiens.  
XX  
PN US2002164679-A1.  
XX  
PD 07-NOV-2002.  
XX  
PF 20-SEP-1999; 99US-00398902.  
XX  
PR 20-MAR-1998; 98WO-GB000677.  
XX  
PA (LUNEC) LUNEC J.  
PA (BEVA/) BEVAN R.  
PA (GRIF/) GRIFFITHS H.  
XX  
PI Lunec J, Bevan R, Griffiths H;  
XX  
XX WPI; 2003-328393/31.  
XX  
DR  
XX  
PT New molecule useful for diagnosing oxidized low density lipoprotein  
XX  
XX (LDL), and for inhibiting the uptake of LDL by high affinity LDL  
XX  
XX receptor, or its partially modified form.  
XX  
PS Claim 1; Page 3; 8pp; English.  
XX  
CC The invention describes a molecule (I) inhibiting uptake by the high  
CC affinity low density lipoprotein (LDL) receptor of LDL or its partially  
CC modified form. (I) And an antibody (II) that binds (I) are useful in the  
CC manufacture of a medicament for inhibiting uptake by the high affinity  
CC LDL receptor of LDL or a partially modified form of it. (I) And (II) are  
CC useful in the diagnostic test for oxidized LDL, or antibody specific  
CC against oxidized LDL, which will cause uptake by the high affinity LDL  
CC receptor of LDL or a partially modified form of it, by: (a) reacting (I)  
CC or (II) with a sample; (b) detecting an antibody-antigen binding reaction  
CC; and (c) correlating the detection of the antibody-antigen binding  
CC reaction with the presence of oxidized LDL, or antibody specific against  
CC oxidized LDL, which will cause uptake by the high affinity LDL receptor  
CC of LDL or a partially modified form of it. (I) Is useful as an immunogen,  
CC e.g., for the production of antibodies, and particularly in the treatment  
CC and diagnosis of atherosclerosis. (I) And (II) are useful as reagents in  
CC diagnostic tests, and for preventing foam cell formation. This is the  
CC amino acid sequence of residues 3359-3369 of Apoprotein B 100 used to  
CC inhibit uptake of the high affinity low density lipoprotein (LDL) by the  
CC LDL receptor  
XX  
SQ Sequence 11 AA;

Query Match 100.0%; Score 44; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.089;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLTRKRGGLK 9  
| | | | |  
DB 1 RLTRKRGGLK 9

RESULT 6  
ADF56451  
ID ADF56451 standard; peptide; 11 AA.

AC ADF56451;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human apolipoprotein B 100 fragment #2.  
 KW human; apolipoprotein B 100; malondialdehyde; MDA;  
 KM low density lipoprotein; high affinity LDL receptor;  
 XX high affinity LDL uptake inhibitor; atherosclerosis.  
 OS Homo sapiens.  
 XX  
 PN US2003157567-A1.  
 XX  
 PD 21-AUG-2003.  
 XX  
 PF 05-FEB-2003; 2003US-00358594.  
 XX  
 PR 20-SEP-1999; 99US-00398902.  
 XX  
 PA (LUNE/) LUNEC J.  
 PA (BEVA/) BEVAN R.  
 PA (GRIF/) GRIFFITHS H.  
 XX  
 PI Lunec J, Bevan R, Griffiths H.  
 DR WPI; 2003-697154/66.  
 XX  
 PT New molecule, useful for treating and diagnosing atherosclerosis,  
 PT comprises 11 amino acid sequence conjugated with malondialdehyde and  
 PT inhibits low density lipoprotein receptor.  
 PS Claim 2; SEQ ID NO 2; 8pp; English.  
 XX  
 CC The invention relates to a molecule comprising one of three fully defined  
 CC amino acid sequences or its partially modified form or analogue, where  
 CC lysine is conjugated with malondialdehyde (MDA) and inhibits uptake by  
 CC the high affinity low density lipoprotein (LDL) receptor or its partially  
 CC human or animal body and in the manufacture of a medicament for  
 CC inhibiting uptake by the high affinity LDLR or its partially modified  
 CC form. The molecule is useful in a diagnostic test method for antibody  
 CC specific against oxidised LDL or oxidised LDL respectively, which will  
 CC cause uptake by the high affinity LDLR or its partially modified  
 CC the molecules and antibodies are for diagnosing and treating  
 CC atherosclerosis. The present sequence represents a human apolipoprotein B  
 CC 100 fragment.  
 XX  
 SQ Sequence 11 AA;  
 Query Match  
 Best Local Similarity 100.0%; Score 44; DB 7; Length 11;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RLTRKRGILK 9  
 DB 1 RLTRKRGILK 9  
 XX  
 DE 19-MAY-1998 (first entry)  
 XX  
 DE Apolipoprotein B-100 fragment.  
 KW Anti-coagulant; apolipoprotein B-100; apob-100; metastatic spread;  
 KM thromboplastin-mediated process; cancer; inhibitor; blood coagulation;  
 KM angiogenesis; cellular differentiation; apoptosis; KRAD-14;  
 KM prothrombinase complex.

XX  
 OS Synthetic.  
 OS Homo sapiens.  
 PN WO9743311-A1.  
 XX  
 PD 20-NOV-1997.  
 XX  
 PF 09-MAY-1997; 97WO-GB001255.  
 XX  
 FR 09-MAY-1996; 96GB-00009702.  
 XX  
 PA (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.  
 XX  
 PI Bruckdorfer KR, Ettele C;  
 DR WPI; 1998-008798/01.  
 XX  
 PT Peptide fragments of apo:apo:protein B-100 with anticoagulant activity -  
 PT used for treating or preventing coagulation, inhibiting angiogenesis,  
 PT cell differentiation and apoptosis.  
 PS Disclosure; Page 9; 60pp; English.  
 XX  
 CC This sequence is an example of the peptide of the invention. It has the  
 CC formula (I) or their variants with one or more internal deletions,  
 CC insertions or substitutions, while retaining anti-coagulant properties,  
 CC apolipoprotein B-100 (apob-100). Z1-KAO-X1-KIKKRRHS-X2-1-22 (I) X1 = S or  
 CC (aa); Z2 = the C terminus of the peptide, a terminal amide group or 1-77  
 CC separate or sequential treatment of cancer, particularly to prevent  
 CC metastatic spread. They are also used to inhibit thromboplastin-mediated  
 CC processes, specifically to prevent or reduce blood coagulation (e.g.  
 CC during or after surgery or in cases of heart attack, stroke etc.) and to  
 CC inhibit angiogenesis, cellular differentiation or apoptosis. KRAD-14,  
 CC which is active as such or as part of a 98-aa peptide, inhibits  
 CC activation of the prothrombinase complex, and prevents activation of  
 CC factor VII on the surface of thromboplastin and of platelets by thrombin.  
 CC It binds to the residues 58-66 of thromboplastin. Since (I) are much  
 CC smaller than apob-100, they act more quickly  
 XX  
 SQ Sequence 12 AA;  
 Query Match  
 Best Local Similarity 100.0%; Score 44; DB 2; Length 12;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RLTRKRGILK 9  
 DB 1 RLTRKRGILK 9  
 XX  
 DE 03-AUG-1998 (first entry)  
 XX  
 DE Apo B 100 binding site peptide analogue peptide B.  
 KW Apo B; binding site; receptor; cancer; drug delivery; anticancer;  
 KM growth supplement; non-natural lipid particle; low density lipoprotein;  
 KM LDL; receptor component; apo B100 receptor site.  
 OS Synthetic.  
 XX  
 FT Key  
 FT Modified-site 1 Location/Qualifiers  
 FT /note="attached to retinoic acid"

PN WO9813385-A2.  
 XX  
 XX 02-APR-1998.  
 XX  
 XX 25-SEP-1997; 97WO-GB002610.  
 XX  
 XX 27-SEP-1996; 96GB-00020153.  
 XX  
 XX (UYST ) UNIV STRATHCLYDE.  
 XX  
 XX Halbert GW, Owens MD, Baillie G;  
 XX  
 XX WPI, 1998-230637/20.  
 XX  
 XX  
 XX Non-natural lipid particle comprising peptide binding to apo B protein  
 XX receptor - useful as, e.g. vector for delivering drugs to cancer cells  
 XX that express this receptor.  
 XX  
 XX  
 XX Claim 13; Fig 7; 73pp; English.  
 XX  
 XX The present sequence represents a specifically claimed Apo B 100 binding  
 XX site peptide analogue which can be used as a component of a non-  
 XX naturally occurring, receptor-competent low density lipoprotein (LDL)  
 XX particle of the present invention. The LDL particle comprises at least 1  
 XX peptide component that has at least 1 binding site for an apo B protein  
 XX receptor and at least 1 lipophilic substituent. Also described in the  
 XX invention are peptides containing an apo B binding sequence with at least  
 XX 70% identity with sequences: KAEYKKNKRRH (1) or TRRLTRKRGK (2), or their  
 XX dimers. Non-naturally occurring, receptor-competent LDL particles are  
 XX useful as: (i) drug-targeting vectors for delivering anticancer drugs to  
 XX cancer cells that express an apo B protein receptor, and (ii) additives  
 XX for cell culture media especially as growth supplements. Non-naturally  
 XX occurring, receptor-competent LDL particles do not require the complete  
 XX apo B sequence, which is large and tends to aggregate, to provide binding  
 XX affinity to an apo B protein receptor  
 XX  
 XX Sequence 13 AA;  
 XX  
 XX  
 XX Query Match 100.0%; Score 44; DB 2; Length 13;  
 XX Best Local Similarity 100.0%; Pred. No. 0.1;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX  
 XX 1 RLTRKRGK 9  
 XX |||||||  
 XX Db 4 RLTRKRGK 12  
 XX  
 XX  
 XX RESULT 9  
 XX AAW22911  
 XX ID AAW22911 standard; peptide; 15 AA.  
 XX  
 XX AAW22911;  
 XX  
 XX 02-OCT-1997 (first entry)  
 XX  
 XX Low density lipoprotein binding peptide.  
 XX  
 XX Low density lipoprotein; LDL; binding; absorbent; removal; body fluid;  
 XX reagent.  
 XX  
 XX Synthetic.  
 XX  
 XX WO9700889-A1.  
 XX  
 XX 09-JAN-1997.  
 XX  
 XX 21-JUN-1996; 96WO-JP001734.  
 XX  
 XX 21-JUN-1995; 95JP-00176904.  
 XX  
 XX (ASAH ) ASAH KASEI KOGYO KK.  
 XX (ASAH ) ASAH MEDICAL CO LTD.  
 XX

PI Hatanaka Y, Aritomi M;  
 XX  
 XX WPI, 1997-087320/08.  
 XX  
 XX Peptide binding to low density lipoprotein - useful in removing LDL from  
 XX body fluids and as carrier peptide(s) for drugs.  
 XX  
 XX  
 XX Example 10; Page 38; 61pp; Japanese.  
 XX  
 XX The present low density lipoprotein (LDL) binding peptide can be used as  
 XX an absorbent to remove LDL from body fluids, or as a LDL binding reagent.  
 XX The peptide can be prepared easily and at low cost, and has excellent  
 XX stability and preservability. It specifically binds LDL, and does not  
 XX cause bradykinin production, white blood cell activation or blood  
 XX agglutination  
 XX  
 XX Sequence 15 AA;  
 XX  
 XX  
 XX Query Match 100.0%; Score 44; DB 2; Length 15;  
 XX Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX  
 XX 1 RLTRKRGK 9  
 XX |||||||  
 XX Db 4 RLTRKRGK 12  
 XX  
 XX  
 XX RESULT 10  
 XX AAW41261  
 XX ID AAW41261 standard; peptide; 15 AA.  
 XX  
 XX AAW41261;  
 XX  
 XX 19-MAY-1998 (first entry)  
 XX  
 XX Apolipoprotein B-100 fragment.  
 XX  
 XX  
 XX Anti-coagulant; apolipoprotein B-100; apob-100; metastatic spread;  
 XX thromboplastin-mediated process; cancer; inhibitor; blood coagulation;  
 XX angiogenesis; cellular differentiation; apoptosis; KRAD-14;  
 XX prothrombinase complex.  
 XX  
 XX Synthetic.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO9743311-A1.  
 XX  
 XX 20-NOV-1997.  
 XX  
 XX 09-MAY-1997; 97WO-GB001255.  
 XX  
 XX 09-MAY-1996; 96GB-00009702.  
 XX  
 XX (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.  
 XX  
 XX Bruckdorfer KR, Ectelate C;  
 XX  
 XX WPI, 1998-008798/01.  
 XX  
 XX Peptide fragments of apo:lipoprotein B-100 with anticoagulant activity -  
 XX used for treating or preventing coagulation, inhibiting angiogenesis,  
 XX cell differentiation and apoptosis.  
 XX  
 XX Disclosure; Page 22; 60pp; English.  
 XX  
 XX This sequence is an example of the peptide of the invention. It has the  
 XX formula (I), or their variants with one or more internal deletions,  
 XX insertions or substitutions, while retaining anti-coagulant properties of  
 XX apolipoprotein B-100 (apob-100). Z1-KAQ-XI-KKNKRRHS-X2-T-Z2 (I) X1 = S or  
 XX Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids  
 XX (aa); Z2 = the C terminus of the peptide, a terminal amide group or 1-77  
 XX aa. Compositions containing the peptide are used for simultaneous,  
 XX separate or sequential treatment of cancer, particularly to prevent

CC metastatic spread. They are also used to inhibit thromboplastin-mediated  
CC processes, specifically to prevent or reduce blood coagulation (e.g.,  
CC inhibiting or after surgery or in cases of heart attack, stroke etc.) and to  
CC inhibit angiogenesis, cellular differentiation or apoptosis (e.g.,  
CC activation of the prothrombinase complex; a peptide, inhibits  
CC factor VII on the surface of thromboplastin and prevents activation of  
CC it binds to the residues 58-66 of thromboplastin and of platelets by thrombin.  
CC smaller than apob-100, they act more quickly  
SQ Sequence 15 AA;

Query Match  
Best Local Similarity 100.0%; Score 44; DB 2; Length 15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RLTTRKGLK 9  
DB 2 RLTTRKGLK 10

RESULT 11

ID AAM96892 standard; peptide; 15 AA.  
XX AAM96892;  
AC AAM96892;  
XX 22-APR-1999 (first entry)  
DE APOB-100 nuclear localisation signal sequence, residues 3353-3367.  
XX Human apolipoprotein B-100; apob-100; very-low density lipoprotein; VLDL;  
KW apolipoprotein; binding; in vivo transport; nuclear acid; binding domain;  
KW non-small cell lung carcinoma; diabetes; arteriosclerosis.  
OS Homo sapiens.  
PN WO965638-A1.  
XX 17-DEC-1998.  
PD 10-JUN-1998; 98WO-US011927.  
XX 13-JUN-1997; 97US-00874807.  
PR 14-MAY-1998; 98US-00079030.  
XX (BAYU) BAYLOR COLLEGE MEDICINE.  
XX Guevara JG, Hoogveen RC, Moore JP;  
DR WPI; 1999-070331/06.  
XX Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -  
PT used for delivering nucleic acid to cells for gene therapy and antisense  
XX treatment.  
XX Claim 19; Fig 13D; 293pp; English.  
XX AAM96878-97 represent nuclear localisation signal sequence derived from  
CC human apolipoprotein B-100 (apob-100). Apob-100 is a major apoprotein  
CC component of very-low density lipoproteins (VLDL); intermediate density  
CC lipoprotein (IDL); low density lipoproteins (LDL); and lipoprotein a.  
CC The composition describes a composition of the invention. The  
CC apolipoprotein is used to deliver nucleic acids to eukaryotic cells.  
CC The molecule is used to deliver nucleic acids to eukaryotic cells.  
CC The molecule (or ribozyme). Specifying a therapeutic polypeptide or antisense  
CC fibrosis and arteriosclerosis. Specifically they are used for gene therapy of  
SQ Sequence 15 AA;

Query Match  
Best Local Similarity 100.0%; Score 44; DB 2; Length 15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RLTTRKGLK 9  
DB 7 RLTTRKGLK 15

RESULT 12

ID ABJ37575 standard; peptide; 20 AA.  
XX ABJ37575;  
AC ABJ37575;  
XX 10-MAY-2003 (first entry)  
DE Heparin binding peptide sequence #28.  
XX Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological.  
KW cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour;  
KW rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.  
OS Undifferentiated.  
PN WO2003007689-A2.  
XX 30-JAN-2003.  
PD 22-JUL-2002; 2002WO-US023419.  
XX 20-JUL-2001; 2001US-0306726P.  
PR (ETHZ-) ETH ZUERICH.  
XX (OYZU-) UNIV ZURICH.  
XX Hubbell JA, Schoenmakers R, Maynard HD;  
DR WPI; 2003-300420/29.  
XX Use of a ligand comprising of at least one sulfated or sulfonated amino  
PT acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic  
XX retinopathy and hypoxia.  
XX Disclosure; Fig 2; 79pp; English.  
XX The invention relates to a novel ligand for binding a target biomolecule,  
CC which comprises a peptide having at least one sulphated or sulfonated  
CC amino acid and at least one amino acid chosen from neutral and positively  
CC charged amino acids. The novel ligands can be used for neutral and positively  
CC charged amino acids. The novel ligands can be used for neutral and positively  
CC charged amino acids. The novel ligands can be used for neutral and positively  
XX charged amino acids. The novel ligands can be used for neutral and positively  
XX charged amino acids. The novel ligands can be used for neutral and positively  
SQ Sequence 20 AA;

Query Match  
Best Local Similarity 100.0%; Score 44; DB 6; Length 20;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RLTTRKGLK 9  
DB 8 RLTTRKGLK 16

RESULT 13

ID AAM57208 standard; peptide; 22 AA.  
XX AAM57208;  
AC AAM57208;  
XX 03-AUG-1998 (first entry)  
DT

```

XX Apo B 100 binding site peptide analogue peptide C.
DE
XX Apo B; binding site; receptor; cancer; drug delivery; anticancer;
XX growth supplement; non-natural lipid particle; low density lipoprotein;
XX LDL; receptor component; apo B100 receptor site.
XX Synthetic.
OS
XX Key Location/Qualifiers
XX Modified-site 1 /note= "attached to retinoic acid"
XX Modified-site 22 /note= "attached to cholesterol"
XX
XX WO9813385-A2.
XX
XX 02-APR-1998.
XX
XX 25-SEP-1997; 97WO-GB002610.
XX
XX 27-SEP-1996; 96GB-00020153.
XX
XX (UYST ) UNIV STRATHCLYDE.
XX
XX Halbert GW, Owens MD, Baillie G;
XX
XX WPI; 1998-230637/20.
XX
XX Non-natural lipid particle comprising peptide binding to apo B protein
XX receptor - useful as, e.g. vector for delivering drugs to cancer cells
XX that express this receptor.
XX
XX Claim 13; Fig 7; 73pp; English.
XX
XX The present sequence represents a specifically claimed Apo B 100 binding
XX site peptide analogue which can be used as a component of a non-
XX naturally occurring, receptor-competent low density lipoprotein (LDL)
XX particle of the present invention. The LDL particle comprises at least 1
XX peptide component that has at least 1 binding site for an apo B protein
XX receptor and at least 1 lipophilic substituent. Also described in the
XX invention are peptides containing an apo B binding sequence with at least
XX 70% identity with sequences: KAEYKKNKRRH (1) or TPTLRKRGKX (2), or their
XX dimers. Non-naturally occurring, receptor-competent LDL particles are
XX useful as: (i) drug-targeting vectors for delivering anticancer drugs to
XX cancer cells that express an apo B protein receptor, and (ii) additives
XX for cell culture media especially as growth supplements. Non-naturally
XX occurring, receptor-competent LDL particles do not require the complete
XX apo B sequence, which is large and tends to aggregate, to provide binding
XX affinity to an apo B protein receptor
XX
XX Sequence 22 AA;
SQ
Query Match 100.0%; Score 44; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLTRKRGKX 9
Db 8 RLTRKRGKX 16

```

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XX growth supplement; non-natural lipid particle; low density lipoprotein;
XX LDL; receptor component; apo B100 receptor site.
XX Synthetic.
OS
XX Key Location/Qualifiers
XX Modified-site 1 /note= "attached to retinoic acid"
XX
XX WO9813385-A2.
XX
XX 02-APR-1998.
XX
XX 25-SEP-1997; 97WO-GB002610.
XX
XX 27-SEP-1996; 96GB-00020153.
XX
XX (UYST ) UNIV STRATHCLYDE.
XX
XX Halbert GW, Owens MD, Baillie G;
XX
XX WPI; 1998-230637/20.
XX
XX Non-natural lipid particle comprising peptide binding to apo B protein
XX receptor - useful as, e.g. vector for delivering drugs to cancer cells
XX that express this receptor.
XX
XX Claim 13; Fig 7; 73pp; English.
XX
XX The present sequence represents a specifically claimed Apo B 100 binding
XX site peptide analogue which can be used as a component of a non-
XX naturally occurring, receptor-competent low density lipoprotein (LDL)
XX particle of the present invention. The LDL particle comprises at least 1
XX peptide component that has at least 1 binding site for an apo B protein
XX receptor and at least 1 lipophilic substituent. Also described in the
XX invention are peptides containing an apo B binding sequence with at least
XX 70% identity with sequences: KAEYKKNKRRH (1) or TPTLRKRGKX (2), or their
XX dimers. Non-naturally occurring, receptor-competent LDL particles are
XX useful as: (i) drug-targeting vectors for delivering anticancer drugs to
XX cancer cells that express an apo B protein receptor, and (ii) additives
XX for cell culture media especially as growth supplements. Non-naturally
XX occurring, receptor-competent LDL particles do not require the complete
XX apo B sequence, which is large and tends to aggregate, to provide binding
XX affinity to an apo B protein receptor
XX
XX Sequence 22 AA;
SQ
Query Match 100.0%; Score 44; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLTRKRGKX 9
Db 8 RLTRKRGKX 16

```

```

RESULT 14
AAW57209
ID AAW57209 standard; peptide; 22 AA.
XX
XX AAW57209;
XX
XX 03-AUG-1998 (first entry)
XX
XX Apo B 100 binding site peptide analogue peptide D.
XX
XX Apo B; binding site; receptor; cancer; drug delivery; anticancer;
XX

```

```

RESULT 15
ABR57177
ID ABR57177 standard; peptide; 23 AA.
XX
XX ABR57177;
XX
XX 29-AUG-2003 (first entry)
XX
XX Human PDGFR-beta related navigation peptide SEQ ID NO:25.
XX
XX PDGFR-beta; platelet derived growth factor receptor beta; nanoparticle;
XX delivery; encapsulated molecule; cytosolic; antitumor; gene therapy;
XX sustained delivery; cell proliferation disorder; infectious disease;
XX genetic defect; aberrant gene regulation.
XX
XX Homo sapiens.
XX

```



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OM protein - protein search, using sw model

Run on: January 12, 2005, 13:14:21 ; Search time 21.1935 Seconds  
(without alignments)  
28.162 Million cell updates/sec

Title: US-10-657-404A-8

Perfect score: 44

Sequence: 1 RLTRKRGK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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- 2: /cgn2\_6/ptodata/1/1aa/5B COMB.pdp:\*
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- 4: /cgn2\_6/ptodata/1/1aa/6B COMB.pdp:\*
- 5: /cgn2\_6/ptodata/1/1aa/PTUS COMB.pdp:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfilest.pdp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	10	4	US-09-265-222-20
2	44	100.0	11	4	US-09-269-533A-2
3	44	100.0	11	4	US-09-269-533A-3
4	44	100.0	12	4	US-09-180-422B-13
5	44	100.0	13	4	US-09-269-533A-4
6	44	100.0	15	3	US-08-981-122-85
7	44	100.0	15	4	US-09-180-422B-17
8	44	100.0	15	4	US-09-079-030-205
9	44	100.0	22	4	US-09-269-533A-5
10	44	100.0	22	4	US-09-269-533A-6
11	44	100.0	36	4	US-09-079-030-166
12	44	100.0	51	4	US-09-079-030-98
13	44	100.0	377	1	US-07-959-946-1
14	44	100.0	377	1	US-08-333-577-1
15	44	100.0	377	5	PCT-US92-08634-1
16	44	100.0	420	4	US-09-079-030-223
17	44	100.0	773	4	US-09-079-030-215
18	44	100.0	840	4	US-09-079-030-214
19	44	100.0	4536	4	US-09-180-422B-27
20	44	100.0	4536	4	US-09-079-030-1
21	44	100.0	4563	4	US-09-108-006C-1
22	44	100.0	4563	4	US-09-538-092-842
23	40	90.9	10	4	US-09-265-222-1
24	40	90.9	10	4	US-09-265-222-6
25	39	88.6	10	4	US-09-265-222-5
26	39	88.6	10	4	US-09-265-222-7
27	39	88.6	10	4	US-09-265-222-9

28	39	88.6	10	4	US-09-265-222-11	Sequence 11, Appl
29	39	88.6	10	4	US-09-265-222-12	Sequence 12, Appl
30	38	86.4	10	4	US-09-265-222-2	Sequence 2, Appl
31	38	86.4	10	4	US-09-265-222-3	Sequence 3, Appl
32	38	86.4	10	4	US-09-265-222-4	Sequence 4, Appl
33	38	86.4	785	4	US-09-079-030-216	Sequence 216, App
34	37	84.1	10	4	US-09-265-222-8	Sequence 8, Appl
35	37	84.1	10	4	US-09-265-222-10	Sequence 10, Appl
36	35	79.5	336	4	US-09-489-039A-13630	Sequence 13630, A
37	35	76.1	11	4	US-09-265-222-16	Sequence 16, Appl
38	33.5	76.1	11	4	US-09-265-222-17	Sequence 17, Appl
39	33.5	76.1	11	4	US-09-265-222-18	Sequence 18, Appl
40	33.5	76.1	11	4	US-09-265-222-19	Sequence 19, Appl
41	33	75.0	676	1	US-08-343-785-2	Sequence 2, Appl
42	33	75.0	676	1	US-08-343-785-8	Sequence 8, Appl
43	33	75.0	676	2	US-08-462-221-2	Sequence 2, Appl
44	33	75.0	676	2	US-08-462-221-8	Sequence 8, Appl
45	33	75.0	676	3	US-08-946-458-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-09-265-222-20  
Sequence 20, Application US/09265222  
Patent No. 6579682  
GENERAL INFORMATION:  
APPLICANT: Innerearity, Thomas  
TITLE OF INVENTION: COMPOUNDS AND TOOLS FOR IDENTIFYING  
TITLE OF INVENTION: COMPOUNDS WHICH MODULATE ATHEROSCLEROSIS BY IMPACTING  
FILE REFERENCE: 22002059700  
CURRENT FILING DATE: 1999-03-05  
PRIOR APPLICATION NUMBER: US/09/265, 222  
PRIOR FILING DATE: 1998-03-10  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 20  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: BINDING  
LOCATION: (1)...(10)  
OTHER INFORMATION: Putative proteoglycan binding site of wild-type  
OTHER INFORMATION: human apo-B100 protein  
US-09-265-222-20  
Query Match 100.0%; Score 44; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 RLTRKRGK 9  
Db 2 RLTRKRGK 10  
RESULT 2  
US-09-269-533A-2  
Sequence 2, Application US/09269533A  
Patent No. 6670452  
GENERAL INFORMATION:  
APPLICANT: University of Strathclyde  
APPLICANT: Owens, Moira  
APPLICANT: Ballie, George  
TITLE OF INVENTION: US 6670452-Naturally Occurring Lipoprotein Particle  
FILE REFERENCE: P0786556  
CURRENT APPLICATION NUMBER: US/09/269, 533A  
CURRENT FILING DATE: 1999-06-01

;; PRIOR APPLICATION NUMBER: PCT/GB97/02610  
;; PRIOR FILING DATE: 1997-09-25  
;; PRIOR APPLICATION NUMBER: GB 9620153.8  
;; NUMBER OF SEQ ID NOS: 7  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO: 2  
;; LENGTH: 11  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1..7)  
;; OTHER INFORMATION: Apo B binding site sequence  
US-09-269-533A-2

Query Match  
Best Local Similarity 100.0%; Score 44; DB 4; Length 11;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RLTRRGGLK 9  
Db 3 RLTRRGGLK 11

RESULT 3  
US-09-269-533A-3  
;; Sequence 3, Application US/09269533A  
;; Patent No. 6670452  
;; GENERAL INFORMATION:  
;; APPLICANT: University of Strathclyde  
;; APPLICANT: Halbert, Gavin  
;; APPLICANT: Owens, Moira  
;; TITLE OF INVENTION: No. 6670452-Naturally Occurring Lipoprotein Particle  
;; FILE REFERENCE: P07885US  
;; CURRENT APPLICATION NUMBER: US/09/269,533A  
;; PRIOR FILING DATE: 1999-06-01  
;; PRIOR APPLICATION NUMBER: PCT/GB97/02610  
;; PRIOR FILING DATE: 1997-09-25  
;; PRIOR APPLICATION NUMBER: GB 9620153.8  
;; NUMBER OF SEQ ID NOS: 7  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO: 3  
;; LENGTH: 11  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1..7)  
;; OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1..7)  
;; OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue  
US-09-269-533A-3

Query Match  
Best Local Similarity 100.0%; Score 44; DB 4; Length 11;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RLTRRGGLK 9  
Db 2 RLTRRGGLK 10

RESULT 4  
US-09-180-422B-13  
;; Sequence 13, Application US/09180422B  
;; Patent No. 644644

;; GENERAL INFORMATION:  
;; APPLICANT: BRUCKDORFER, KARL R  
;; TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED  
;; NUMBER OF SEQUENCES: 27  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESS: NIXON & VANDERHAYE, P.C.  
;; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
;; CITY: ARLINGTON  
;; STATE: VA  
;; COUNTRY: USA  
;; ZIP: 22201  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: IBM PC compatible  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/180,422B  
;; FILING DATE: 07-Dec-1998  
;; CLASSIFICATION: <Unknown>  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: SADOFF, B.J.  
;; REGISTRATION NUMBER: 36663  
;; REFERENCE/DOCKET NUMBER: 117-268  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 7038164000  
;; INFORMATION FOR SEQ ID NO: 13:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 12 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-180-422B-13

Query Match  
Best Local Similarity 100.0%; Score 44; DB 4; Length 12;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RLTRRGGLK 9  
Db 1 RLTRRGGLK 9

RESULT 5  
US-09-269-533A-4  
;; Sequence 4, Application US/09269533A  
;; Patent No. 6670452  
;; GENERAL INFORMATION:  
;; APPLICANT: University of Strathclyde  
;; APPLICANT: Halbert, Gavin  
;; APPLICANT: Owens, Moira  
;; TITLE OF INVENTION: No. 6670452-Naturally Occurring Lipoprotein Particle  
;; FILE REFERENCE: P07885US  
;; CURRENT APPLICATION NUMBER: US/09/269,533A  
;; PRIOR FILING DATE: 1999-06-01  
;; PRIOR APPLICATION NUMBER: PCT/GB97/02610  
;; PRIOR FILING DATE: 1997-09-25  
;; PRIOR APPLICATION NUMBER: GB 9620153.8  
;; NUMBER OF SEQ ID NOS: 7  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO: 4  
;; LENGTH: 13  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; NAME/KEY: misc\_feature

LOCATION: ( )  
 OTHER INFORMATION: Synthesized peptide analogue of the Apo B 100 binding site  
 NAME/KEY: misc:feature  
 LOCATION: ( )  
 OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue  
 US-09-269-533A-4

Query Match 100.0%; Score 44; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.034;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRKRGK 9  
 |||||  
 Db 4 RLTRKRGK 12

RESULT 6  
 US-08-981-122-85  
 Sequence 85, Application US/08981122B  
 Patent No. 6127339

GENERAL INFORMATION:  
 APPLICANT: Hatanaka, Yoshihiro  
 APPLICANT: Aritomi, Masaharu  
 TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein  
 FILE REFERENCE:  
 CURRENT APPLICATION NUMBER: US/08/981,122B  
 CURRENT FILING DATE: 1997-12-18  
 PRIOR APPLICATION NUMBER: JP 7-176904  
 PRIOR FILING DATE: 1995-06-21  
 PRIOR APPLICATION NUMBER: PCT/JP96/01734  
 PRIOR FILING DATE: 1996-06-21  
 NUMBER OF SEQ ID NOS: 90  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO 85  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Sequence of a peptide synthesized in Comparative Example 7 from  
 Patent No. 6127339  
 OTHER INFORMATION: L-form F-moc amino acids by solid phase method using an  
 OTHER INFORMATION: automatic peptide synthesizer (9050 plus peptide synthesizer)  
 PUBLICATION INFORMATION:  
 AUTHORS: Urban Olsson et al.  
 TITLE: Binding of a synthetic apolipoprotein B-100 peptide and peptide  
 TITLE: analogues to chondroitin 6-sulfate: Effects of the lipid environment  
 JOURNAL: Biochemistry  
 VOLUME: 32  
 PAGES: 1858-1865  
 US-08-981-122-85

Query Match 100.0%; Score 44; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.039;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRKRGK 9  
 |||||  
 Db 4 RLTRKRGK 12

RESULT 7  
 US-09-180-422B-17  
 Sequence 17, Application US/09180422B  
 Patent No. 6444644

GENERAL INFORMATION:  
 APPLICANT: BRUCKDORFER, KARL R  
 ETTELAIE, CAMILLE  
 TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED  
 FROM APOLOPROTEIN B-100  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHAY, P.C.  
 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR

CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22201  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/180,422B  
 FILING DATE: 07-Dec-1998  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SADOFF, B.J.  
 REGISTRATION NUMBER: 36663  
 REFERENCE/DOCKET NUMBER: 117-268  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 7038164000  
 TELEFAX: 7038164100  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
 US-09-180-422B-17

Query Match 100.0%; Score 44; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.039;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRKRGK 9  
 |||||  
 Db 2 RLTRKRGK 10

RESULT 8  
 US-09-079-030-205  
 Sequence 205, Application US/09079030  
 Patent No. 6635623  
 GENERAL INFORMATION:  
 APPLICANT: Guevera, Jr., Juan G.  
 APPLICANT: Hoogeveen, Ron C.  
 APPLICANT: Moore, Paul J.  
 TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY  
 TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS  
 NUMBER OF SEQUENCES: 229  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Arnold, White & Durkee  
 STREET: P.O. Box 4433  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: USA  
 ZIP: 77210  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/079,030  
 FILING DATE: Concurrently Herewith  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McMillian, Nabesla R.  
 REGISTRATION NUMBER: P-43,363  
 REFERENCE/DOCKET NUMBER: ARA0:003  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 512/418-3000  
 TELEFAX: 512/474-7577

; INFORMATION FOR SEQ ID NO: 205:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-09-079-030-205

Query Match  
Best Local Similarity 100.0%; Score 44; DB 4; Length 15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRRRGLK 9  
DB 7 RLTRRRGLK 15

RESULT 9  
US-09-269-533A-5  
; Sequence 5, Application US/09269533A  
; Patent No. 6670452  
; GENERAL INFORMATION:  
; APPLICANT: University of Strathclyde  
; APPLICANT: Halbert, Gavin  
; APPLICANT: Owens, Moira  
; APPLICANT: Baillie, George  
; TITLE OF INVENTION: No. 6670452-Naturally Occurring Lipoprotein Particle  
; FILE REFERENCE: P07885US  
; CURRENT APPLICATION NUMBER: US/09/269,533A  
; PRIOR FILING DATE: 1999-06-01  
; PRIOR APPLICATION NUMBER: PCT/GB97/02610  
; PRIOR FILING DATE: 1997-09-25  
; PRIOR APPLICATION NUMBER: GB 9620153.8  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue  
US-09-269-533A-5

Query Match  
Best Local Similarity 100.0%; Score 44; DB 4; Length 22;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRRRGLK 9  
DB 8 RLTRRRGLK 16

RESULT 10  
US-09-269-533A-6  
; Sequence 6, Application US/09269533A  
; Patent No. 6670452  
; GENERAL INFORMATION:  
; APPLICANT: University of Strathclyde  
; APPLICANT: Halbert, Gavin  
; APPLICANT: Owens, Moira  
; APPLICANT: Baillie, George  
; TITLE OF INVENTION: No. 6670452-Naturally Occurring Lipoprotein Particle  
; FILE REFERENCE: P07885US  
; CURRENT APPLICATION NUMBER: US/09/269,533A

; CURRENT FILING DATE: 1999-06-01  
; PRIOR APPLICATION NUMBER: PCT/GB97/02610  
; PRIOR FILING DATE: 1997-09-25  
; PRIOR APPLICATION NUMBER: GB 9620153.8  
; PRIOR FILING DATE: 1996-09-27  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue  
US-09-269-533A-6

Query Match  
Best Local Similarity 100.0%; Score 44; DB 4; Length 22;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRRRGLK 9  
DB 8 RLTRRRGLK 16

RESULT 11  
US-09-079-030-166  
; Sequence 166, Application US/09079030  
; Patent No. 6635623  
; GENERAL INFORMATION:  
; APPLICANT: Guevara, Jr., Juan G.  
; APPLICANT: Hoogewegen, Ron C.  
; APPLICANT: Moore, Paul J.  
; TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY  
; NUMBER OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS  
; NUMBER OF SEQUENCES: 229  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079,030  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMillian, Nabeeja R.  
; REGISTRATION NUMBER: P-43,363  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 166:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-09-079-030-166

Query Match  
Best Local Similarity 100.0%; Score 44; DB 4; Length 36;  
Matches 100.0%; Pred. No. 0.089;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRKRGK 9  
| | | | |  
DB 12 RLTRKRGK 20

## RESULT 12

US-09-079-030-98  
; Sequence 98, Application US/09079030  
; Patent No. 6635623  
; GENERAL INFORMATION:  
; APPLICANT: Guevera, Jr., Juan G.  
; APPLICANT: Hoogveen, Ron C.  
; APPLICANT: Moore, Paul J.  
; TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY  
; NUMBER OF SEQUENCES: 229  
; TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079,030  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMillian, Nabuela R.  
; REGISTRATION NUMBER: P-43,363  
; REFERENCE/DOCKET NUMBER: ABAG:003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 98:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 51 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; US-09-079-030-98

Query Match 100.0%; Score 44; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRKRGK 9  
| | | | |  
DB 7 RLTRKRGK 15

RESULT 13  
US-07-959-946-1  
; Sequence 1, Application US/07959946  
; Patent No. 5408038  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Richard K.  
; APPLICANT: Koduri, Raju  
; APPLICANT: Young, Stephen G.  
; APPLICANT: Witzum, Joseph L.  
; APPLICANT: Curtiss, Linda K.  
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a  
; NUMBER OF SEQUENCES: 20  
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutter &

ADDRESSEE: Milnamow, Ltd.  
STREET: 180 No. 5408038th Stetson, Suite 4700  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60601

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/959,946  
; FILING DATE: 19921008  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,706  
; FILING DATE: 18-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gamsen, Edward P.  
; REGISTRATION NUMBER: 29,381  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312)616-5400  
; TELEFAX: (312)616-5460  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 377 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-07-959-946-1

Query Match 100.0%; Score 44; DB 1; Length 377;  
Best Local Similarity 100.0%; Pred. No. 0.81;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRKRGK 9  
| | | | |  
DB 146 RLTRKRGK 154

RESULT 14  
US-08-333-577-1  
; Sequence 1, Application US/08333577  
; Patent No. 5786206  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Richard K.  
; APPLICANT: Koduri, Raju  
; APPLICANT: Young, Stephen G.  
; APPLICANT: Witzum, Joseph L.  
; APPLICANT: Curtiss, Linda K.  
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a  
; NUMBER OF SEQUENCES: 20  
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutter &  
; ADDRESSEE: Milnamow, Ltd.  
; STREET: 180 No. 5786206th Stetson, Suite 4700  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/333,577  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:

NAME: Gamson, Edward P.  
REGISTRATION NUMBER: 29,381  
REFERENCE/DOCKET NUMBER: SCRF 234.0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)616-5400  
TELEFAX: (312)616-5460  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 377 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-333-577-1

Query Match 100.0%; Score 44; DB 1; Length 377;  
Best Local Similarity 100.0%; Pred. No. 0.81;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRRRGLK 9  
|||  
Db 146 RLTRRRGLK 154

## RESULT 15

PCT-US92-08634-1  
Sequence 1, Application PC/TUS9208634  
GENERAL INFORMATION:  
APPLICANT: Smith, Richard K.  
APPLICANT: Koduri, Raju  
APPLICANT: Young, Stephen G.  
APPLICANT: Wiltum, Joseph L.  
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &  
ADDRESSEE: Milanow, Ltd.  
STREET: 180 North Stetson, Suite 4700  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/08634  
FILING DATE: 19921009  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,706  
FILING DATE: 18-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Gamson, Edward P.  
REGISTRATION NUMBER: 29,381  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)616-5400  
TELEFAX: (312)616-5460  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 377 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US92-08634-1

Query Match 100.0%; Score 44; DB 5; Length 377;  
Best Local Similarity 100.0%; Pred. No. 0.81;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRRRGLK 9  
|||  
Db 146 RLTRRRGLK 154

Search completed: January 12, 2005, 13:33:16  
Job time : 21.1935 secs

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OM protein - protein search, using sw model

Run on: January 12, 2005, 13:31:02 ; Search time 72.2903 Seconds

(without alignments)  
44.980 Million cell updates/sec

Title: US-10-657-404A-8

Perfect score: 44

Sequence: 1 RLTRKRGK 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubpaa/US09 NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/1/pubpaa/US10 NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	9	17	US-10-657-404A-8
2	44	100.0	10	9	US-09-823-418-20
3	44	100.0	10	9	US-09-822-965-20
4	44	100.0	11	9	US-09-269-533A-2
5	44	100.0	11	9	US-09-269-533A-3
6	44	100.0	11	9	US-09-398-902-2
7	44	100.0	11	14	US-09-931-375A-76
8	44	100.0	11	14	US-10-358-594-2
9	44	100.0	11	17	US-10-657-404A-2
10	44	100.0	11	17	US-10-657-404A-3
11	44	100.0	13	9	US-09-269-533A-4
12	44	100.0	13	17	US-10-657-404A-4
13	44	100.0	22	9	US-09-269-533A-5

14	44	100.0	22	9	US-09-269-533A-6	Sequence 6, Appli
15	44	100.0	22	17	US-10-657-404A-5	Sequence 5, Appli
16	44	100.0	22	17	US-10-657-404A-6	Sequence 6, Appli
17	44	100.0	25	17	US-10-657-404A-9	Sequence 9, Appli
18	44	100.0	34	15	US-10-333-313-1	Sequence 1, Appli
19	44	100.0	34	15	US-09-864-761-46837	Sequence 46837, A
20	44	100.0	3000	16	US-10-741-601-431	Sequence 431, App
21	44	100.0	4563	9	US-09-870-759-128	Sequence 128, App
22	44	100.0	4563	10	US-09-802-640-32	Sequence 32, Appl
23	44	100.0	4563	10	US-09-751-708A-128	Sequence 128, App
24	44	100.0	4563	14	US-10-403-902A-32	Sequence 32, Appl
25	44	100.0	4563	16	US-10-741-601-432	Sequence 432, App
26	44	100.0	4563	16	US-10-741-601-433	Sequence 433, App
27	44	100.0	4563	17	US-10-428-877A-124	Sequence 124, App
28	40	90.9	10	9	US-09-823-418-1	Sequence 1, Appli
29	40	90.9	10	9	US-09-823-418-6	Sequence 6, Appli
30	40	90.9	10	9	US-09-822-965-1	Sequence 1, Appli
31	40	90.9	10	9	US-09-822-965-6	Sequence 6, Appli
32	39	88.6	10	9	US-09-823-418-5	Sequence 5, Appli
33	39	88.6	10	9	US-09-823-418-7	Sequence 7, Appli
34	39	88.6	10	9	US-09-823-418-9	Sequence 9, Appli
35	39	88.6	10	9	US-09-823-418-11	Sequence 11, Appli
36	39	88.6	10	9	US-09-823-418-12	Sequence 12, Appli
37	39	88.6	10	9	US-09-823-965-5	Sequence 5, Appli
38	39	88.6	10	9	US-09-822-965-7	Sequence 7, Appli
39	39	88.6	10	9	US-09-822-965-9	Sequence 9, Appli
40	39	88.6	10	9	US-09-822-965-11	Sequence 11, Appli
41	39	88.6	10	9	US-09-822-965-12	Sequence 12, Appli
42	38	86.4	10	9	US-09-823-418-2	Sequence 2, Appli
43	38	86.4	10	9	US-09-823-418-3	Sequence 3, Appli
44	38	86.4	10	9	US-09-823-418-4	Sequence 4, Appli
45	38	86.4	10	9	US-09-822-965-2	Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
US-10-657-404A-8  
; Sequence 8, Application US/10657404A  
; Publication No. US20040235730A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Strathclyde  
; APPLICANT: Halbert, Gavin  
; APPLICANT: Owens, Moira  
; TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle  
; FILE REFERENCE: P07885US-CIP  
; CURRENT APPLICATION NUMBER: US/10/657,404A  
; CURRENT FILING DATE: 2003-09-08  
; PRIOR APPLICATION NUMBER: PCT/GB97/02610  
; PRIOR FILING DATE: 1997-09-25  
; PRIOR APPLICATION NUMBER: GB 9620153.8  
; PRIOR FILING DATE: 1996-09-27  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Apo B binding site sequence  
US-10-657-404A-8  
Query Match 100.0%; Score 44; DB 17; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 1 RLTRKRGK 9  
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DB 1 RLTRKRGK 9

RESULT 2  
US-09-823-418-20  
; Sequence 20, Application US/09823418  
; Publication No. US20010024797A1  
; GENERAL INFORMATION:  
; APPLICANT: Innervitaly, Thomas  
; APPLICANT: Innervitaly, Thomas  
; TITLE OF INVENTION: METHODS AND TOOLS FOR IDENTIFYING COMPOUNDS  
; TITLE OF INVENTION: WHICH MODULATE ATHEROSCLEROSIS BY IMPACTING  
; FILE REFERENCE: 220002059711  
; CURRENT APPLICATION NUMBER: US/09/823,418  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: US 09/265,222  
; PRIOR FILING DATE: 1999-03-05  
; PRIOR APPLICATION NUMBER: US 60/077,618  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: BINDING  
; LOCATION: (1)...(10)  
; OTHER INFORMATION: Putative proteoglycan binding site of wild-type  
US-09-823-418-20

Query Match  
Best Local Similarity 100.0%; Score 44; DB 9; Length 10;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RLTRKRGK 9  
Db 2 RLTRKRGK 10

RESULT 3  
US-09-822-965-20  
; Sequence 20, Application US/09822965  
; Publication No. US20010029027A1  
; GENERAL INFORMATION:  
; APPLICANT: Innervitaly, Thomas  
; APPLICANT: Innervitaly, Thomas  
; TITLE OF INVENTION: METHODS AND TOOLS FOR IDENTIFYING  
; TITLE OF INVENTION: COMPOUNDS WHICH MODULATE ATHEROSCLEROSIS BY IMPACTING  
; FILE REFERENCE: 220002059710  
; CURRENT APPLICATION NUMBER: US/09/822,965  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: US 09/265,222  
; PRIOR FILING DATE: 1999-03-05  
; PRIOR APPLICATION NUMBER: US 60/077,618  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: BINDING  
; LOCATION: (1)...(10)  
; OTHER INFORMATION: Putative proteoglycan binding site of wild-type  
US-09-822-965-20

Query Match  
Best Local Similarity 100.0%; Score 44; DB 9; Length 10;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRKRGK 9  
Db 2 RLTRKRGK 10

RESULT 4  
US-09-269-533A-2  
; Sequence 2, Application US/09269533A  
; Patent No. US20020147304A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Strathclyde  
; APPLICANT: Halbert, Gavin  
; APPLICANT: Owens, Moira  
; TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle  
; FILE REFERENCE: P0788505  
; CURRENT APPLICATION NUMBER: US/09/269,533A  
; PRIOR FILING DATE: 1999-06-01  
; PRIOR APPLICATION NUMBER: PCT/GB97/02610  
; PRIOR FILING DATE: 1997-09-25  
; PRIOR APPLICATION NUMBER: GB 9620153.8  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(7)  
; OTHER INFORMATION: Apo B binding site sequence  
US-09-269-533A-2

Query Match  
Best Local Similarity 100.0%; Score 44; DB 9; Length 11;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RLTRKRGK 9  
Db 3 RLTRKRGK 11

RESULT 5  
US-09-269-533A-3  
; Sequence 3, Application US/09269533A  
; Patent No. US20020147304A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Strathclyde  
; APPLICANT: Halbert, Gavin  
; APPLICANT: Owens, Moira  
; TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle  
; FILE REFERENCE: P0788505  
; CURRENT APPLICATION NUMBER: US/09/269,533A  
; PRIOR FILING DATE: 1999-06-01  
; PRIOR APPLICATION NUMBER: PCT/GB97/02610  
; PRIOR FILING DATE: 1997-09-25  
; PRIOR APPLICATION NUMBER: GB 9620153.8  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(7)  
; OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site  
LOCATION: (1)..(7)  
; OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue

Query Match  
Best Local Similarity 100.0%; Score 44; DB 9; Length 11;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NAME/KEY: misc feature  
LOCATION: (1..7)  
OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue  
US-09-269-533A-3

Query Match  
Best Local Similarity 100.0%; Score 44; DB 9; Length 11;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLTRRGGLK 9  
Db 2 RLTRRGGLK 10

RESULT 6  
US-09-398-902-2  
Sequence 2, Application US/09398902  
Patent No. US20020164679A1  
GENERAL INFORMATION:  
APPLICANT: Lunec, Joe  
APPLICANT: Bevan, Ruth  
APPLICANT: Griffiths, Helen  
TITLE OF INVENTION: OXIDISED FRAGMENTS OF APOLIPOPROTEIN B AND THEIR USE  
FILE REFERENCE: 3523P003  
CURRENT APPLICATION NUMBER: US/09/398,902  
CURRENT FILING DATE: 1999-09-20  
PRIOR APPLICATION NUMBER: PCT/GB98/00677  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: GB 9705831.7  
PRIOR FILING DATE: 1997-03-20  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 2  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-398-902-2

Query Match  
Best Local Similarity 100.0%; Score 44; DB 9; Length 11;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLTRRGGLK 9  
Db 1 RLTRRGGLK 9

RESULT 7  
US-09-931-375A-76  
Sequence 76, Application US/09931375A  
Publication No. US20030027151A1  
GENERAL INFORMATION:  
APPLICANT: WARMAN, Matthew L.  
APPLICANT: GONG, Yaogin  
APPLICANT: OLSEN, Bjorn R.  
APPLICANT: RAWADI, Georges  
APPLICANT: ROMAN-ROMAN, Sergio  
TITLE OF INVENTION: REGULATOR GENE AND SYSTEM USEFUL FOR THE DIAGNOSIS AND THERAPY OF  
FILE REFERENCE: 38464-0004  
CURRENT APPLICATION NUMBER: US/09/931,375A  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/304,851  
PRIOR FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: US 60/234,337  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: US 60/226,119  
PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 89  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 76  
LENGTH: 11  
TYPE: PRT

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide that can act as an effector of BSMR  
US-09-931-375A-76

Query Match  
Best Local Similarity 100.0%; Score 44; DB 10; Length 11;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLTRRGGLK 9  
Db 1 RLTRRGGLK 9

RESULT 8  
US-10-358-594-2  
Sequence 2, Application US/10358594  
Publication No. US20030157567A1  
GENERAL INFORMATION:  
APPLICANT: Lunec, Joe  
APPLICANT: Bevan, Ruth  
APPLICANT: Griffiths, Helen  
TITLE OF INVENTION: OXIDISED FRAGMENTS OF APOLIPOPROTEIN B AND THEIR USE  
FILE REFERENCE: 3523P003  
CURRENT APPLICATION NUMBER: US/10/358,594  
CURRENT FILING DATE: 2003-02-05  
PRIOR APPLICATION NUMBER: US/09/398,902  
PRIOR FILING DATE: 1999-09-20  
PRIOR APPLICATION NUMBER: PCT/GB98/00677  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: GB 9705831.7  
PRIOR FILING DATE: 1997-03-20  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 2  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-358-594-2

Query Match  
Best Local Similarity 100.0%; Score 44; DB 14; Length 11;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLTRRGGLK 9  
Db 1 RLTRRGGLK 9

RESULT 9  
US-10-657-404A-2  
Sequence 2, Application US/10657404A  
Publication No. US20040235730A1  
GENERAL INFORMATION:  
APPLICANT: University of Strathclyde  
APPLICANT: Halbert, Gavin  
APPLICANT: Owens, Molra  
APPLICANT: Baillie, George  
TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle  
FILE REFERENCE: P07885US-CIP  
CURRENT APPLICATION NUMBER: US/10/657,404A  
CURRENT FILING DATE: 2003-09-08  
PRIOR APPLICATION NUMBER: PCT/GB97/02610  
PRIOR FILING DATE: 1997-09-25  
PRIOR APPLICATION NUMBER: GB 9620153.8  
PRIOR FILING DATE: 1996-09-27  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 2  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:

/ NAME/KEY: misc feature  
/ OTHER INFORMATION: Apo B binding site sequence  
US-10-657-404A-2

Query Match 100.0%; Score 44; DB 17; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRKRGK 9  
Db 3 RLTRKRGK 11

RESULT 10  
US-10-657-404A-3  
/ Sequence 3, Application US/10657404A  
/ Publication No. US20040235730A1  
/ GENERAL INFORMATION:  
/ APPLICANT: University of Strathclyde  
/ APPLICANT: Halbert, Gavin  
/ APPLICANT: Owens, Moira  
/ APPLICANT: Baillie, George  
/ TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle  
/ FILE REFERENCE: P07885US-CIP  
/ CURRENT APPLICATION NUMBER: US/10/657,404A  
/ PRIOR FILING DATE: 2003-09-08  
/ PRIOR APPLICATION NUMBER: PCT/GB97/02610  
/ PRIOR FILING DATE: 1997-09-25  
/ PRIOR APPLICATION NUMBER: GB 9620153.8  
/ NUMBER OF SEQ ID NOS: 9  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 3  
/ LENGTH: 11  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ NAME/KEY: misc feature  
/ OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site  
/ NAME/KEY: misc feature  
/ OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue  
/ FEATURE:  
/ NAME/KEY: misc feature  
/ OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue  
US-10-657-404A-3

Query Match 100.0%; Score 44; DB 17; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRKRGK 9  
Db 2 RLTRKRGK 10

RESULT 11  
US-09-269-533A-4  
/ Sequence 4, Application US/09269533A  
/ Patent No. US20020147304A1  
/ GENERAL INFORMATION:  
/ APPLICANT: University of Strathclyde  
/ APPLICANT: Halbert, Gavin  
/ APPLICANT: Owens, Moira  
/ APPLICANT: Baillie, George  
/ TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle  
/ FILE REFERENCE: P07885US  
/ CURRENT APPLICATION NUMBER: US/09/269,533A  
/ PRIOR FILING DATE: 1999-06-01  
/ PRIOR APPLICATION NUMBER: PCT/GB97/02610  
/ PRIOR FILING DATE: 1997-09-25  
/ PRIOR APPLICATION NUMBER: GB 9620153.8  
/ PRIOR FILING DATE: 1996-09-27

/ NUMBER OF SEQ ID NOS: 7  
/ SOFTWARE: PatentIn version 3.0  
/ SEQ ID NO 4  
/ LENGTH: 13  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ NAME/KEY: misc feature  
/ LOCATION: ( )..( )  
/ OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site  
/ NAME/KEY: misc feature  
/ LOCATION: ( )..( )  
/ OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue  
US-09-269-533A-4

Query Match 100.0%; Score 44; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRKRGK 9  
Db 4 RLTRKRGK 12

RESULT 12  
US-10-657-404A-4  
/ Sequence 4, Application US/10657404A  
/ Publication No. US20040235730A1  
/ GENERAL INFORMATION:  
/ APPLICANT: University of Strathclyde  
/ APPLICANT: Halbert, Gavin  
/ APPLICANT: Owens, Moira  
/ APPLICANT: Baillie, George  
/ TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle  
/ FILE REFERENCE: P07885US-CIP  
/ CURRENT APPLICATION NUMBER: US/10/657,404A  
/ PRIOR FILING DATE: 2003-09-08  
/ PRIOR APPLICATION NUMBER: PCT/GB97/02610  
/ PRIOR FILING DATE: 1997-09-25  
/ PRIOR APPLICATION NUMBER: GB 9620153.8  
/ NUMBER OF SEQ ID NOS: 9  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 4  
/ LENGTH: 13  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ NAME/KEY: misc feature  
/ OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site  
/ NAME/KEY: misc feature  
/ OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue  
US-10-657-404A-4

Query Match 100.0%; Score 44; DB 17; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRKRGK 9  
Db 4 RLTRKRGK 12

RESULT 13  
US-09-269-533A-5  
/ Sequence 5, Application US/09269533A  
/ Patent No. US20020147304A1  
/ GENERAL INFORMATION:  
/ APPLICANT: University of Strathclyde  
/ APPLICANT: Halbert, Gavin  
/ APPLICANT: Owens, Moira  
/ APPLICANT: Baillie, George

TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle  
 FILE REFERENCE: P07885US  
 CURRENT APPLICATION NUMBER: US/09/269,533A  
 CURRENT FILING DATE: 1999-06-01  
 PRIOR APPLICATION NUMBER: PCT/GB97/02610  
 PRIOR FILING DATE: 1997-09-25  
 PRIOR APPLICATION NUMBER: GB 9620153.8  
 PRIOR FILING DATE: 1996-09-27  
 NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 5  
 LENGTH: 22  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (1..7)  
 OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site  
 NAME/KEY: misc feature  
 LOCATION: (1..7)  
 OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue  
 NAME/KEY: misc feature  
 LOCATION: (1..1)  
 OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue  
 US-09-269-533A-5

Query Match 100.0%; Score 44; DB 9; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.25;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RLTRRGGLK 9  
 |||||  
 Db 8 RLTRRGGLK 16

RESULT 14  
 US-09-269-533A-6  
 Sequence 6, Application US/09269533A  
 Patent No. US20020147304A1  
 GENERAL INFORMATION:  
 APPLICANT: University of Strathclyde  
 APPLICANT: Halbert, Gavin  
 APPLICANT: Owens, Moira  
 APPLICANT: Baillie, George  
 TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle  
 FILE REFERENCE: P07885US  
 CURRENT APPLICATION NUMBER: US/09/269,533A  
 CURRENT FILING DATE: 1999-06-01  
 PRIOR APPLICATION NUMBER: PCT/GB97/02610  
 PRIOR FILING DATE: 1997-09-25  
 PRIOR APPLICATION NUMBER: GB 9620153.8  
 PRIOR FILING DATE: 1996-09-27  
 NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 6  
 LENGTH: 22  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (1..7)  
 OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site  
 NAME/KEY: misc feature  
 LOCATION: (1..1)  
 OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue  
 US-09-269-533A-6

Query Match 100.0%; Score 44; DB 9; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.25;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RLTRRGGLK 9  
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Db 8 RLTRRGGLK 16

RESULT 15  
 US-10-657-404A-5  
 Sequence 5, Application US/10657404A  
 Publication No. US20040235730A1  
 GENERAL INFORMATION:  
 APPLICANT: University of Strathclyde  
 APPLICANT: Halbert, Gavin  
 APPLICANT: Owens, Moira  
 APPLICANT: Baillie, George  
 TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle  
 FILE REFERENCE: P07885US-CIP  
 CURRENT APPLICATION NUMBER: US/10/657,404A  
 CURRENT FILING DATE: 2003-09-08  
 PRIOR APPLICATION NUMBER: PCT/GB97/02610  
 PRIOR FILING DATE: 1997-09-25  
 PRIOR APPLICATION NUMBER: GB 9620153.8  
 PRIOR FILING DATE: 1996-09-27  
 NUMBER OF SEQ ID NOS: 9  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 5  
 LENGTH: 22  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (1..7)  
 OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site  
 NAME/KEY: misc feature  
 LOCATION: (1..7)  
 OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue  
 NAME/KEY: misc feature  
 LOCATION: (1..1)  
 OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue  
 US-10-657-404A-5

Query Match 100.0%; Score 44; DB 17; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.25;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RLTRRGGLK 9  
 |||||  
 Db 8 RLTRRGGLK 16

Search completed: January 12, 2005, 13:52:50  
 Job time : 72.2903 secs



GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: January 12, 2005, 13:13:31 ; Search time 16.5484 Seconds  
(without alignments)  
52.328 Million cell updates/sec

Title: US-10-657-404a-8  
Perfect score: 44  
Sequence: 1 RLTRKRGK 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*

1: PIR1:.\*  
2: PIR2:.\*  
3: PIR3:.\*  
4: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	269	2	C60950
2	44	100.0	596	2	S32802
3	44	100.0	779	2	JH0102
4	44	100.0	4563	1	LPHUB
5	39	88.6	274	2	A60950
6	39	88.6	275	2	B60950
7	38	86.4	784	2	JH0101
8	37	84.1	680	2	AB1875
9	35	79.5	305	2	A75334
10	34	77.3	561	1	S34191
11	33	75.0	107	2	S32607
12	33	75.0	112	2	S33822
13	33	75.0	198	2	T41529
14	33	75.0	259	1	B69407
15	33	75.0	309	2	AH0906
16	33	75.0	401	2	E75213
17	33	75.0	676	2	A40363
18	33	75.0	1058	2	S65460
19	33	75.0	1778	2	U70382
20	33	75.0	2629	2	I46569
21	32	72.7	188	2	F87217
22	32	72.7	197	2	JC4150
23	32	72.7	219	2	A53305
24	32	72.7	258	2	T01873
25	32	72.7	330	1	F89534
26	32	72.7	339	2	F82654
27	32	72.7	363	1	A29376
28	32	72.7	436	2	F86486
29	32	72.7	668	1	S74619

30	32	72.7	1073	2	T01955	hypothetical prote
31	32	72.7	1241	2	H84486	probable helicase
32	32	72.7	1265	2	F84517	probable helicase
33	32	72.7	1678	2	D6481	189.6K hypothetical
34	32	72.7	1752	2	T48965	hypothetical prote
35	31	70.5	84	2	G87376	hypothetical prote
36	31	70.5	168	2	T03168	hypothetical prote
37	31	70.5	228	2	TYMUG1	trichome different
38	31	70.5	232	1	S28609	phosphoadenylyl-su
39	31	70.5	249	2	B82400	tomBI protein VCAO
40	31	70.5	290	2	S39854	crax protein - Scr
41	31	70.5	304	2	A98146	probable threonin
42	31	70.5	309	1	E65112	hypothetical 34.6
43	31	70.5	309	2	B85985	hypothetical prote
44	31	70.5	309	2	B91140	hypothetical prote
45	31	70.5	336	2	AC3142	threonine dehydrat

## ALIGNMENTS

## RESULT 1

C60950  
apolipoprotein B-100 - golden hamster (fragment)  
C:Species: Mesocricetus auratus (golden hamster)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C:Accession: C60950  
R:Law, A.; Scott, J.  
J. Lipid Res. 31, 1109-1120, 1990  
A>Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL  
A:Reference number: A60950; MUID:90324804; PMID:2373961  
A:Accession: C60950  
A:Molecule type: DNA  
A:Residues: 1-269 <LAW>  
A:Cross-references: UNIPROT:Q60537; UNIPROT:Q60536  
C:Superfamily: apolipoprotein B  
C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

Query Match 100.0%; Score 44; DB 2; Length 269;  
Best Local Similarity 100.0%; Pred. No. 0.27;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRKRGK 9

DB 217 RLTRKRGK 225

## RESULT 2

S32802  
apolipoprotein B - crab-eating macaque (fragment)  
C:Species: Macaca fascicularis (crab-eating macaque)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S32802  
R:Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchio  
Biochim. Biophys. Acta 1086, 326-334, 1991  
A>Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional re  
A:Reference number: S32802; MUID:92075708; PMID:1742325  
A:Accession: S32802  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-596 <PAP>  
A:Cross-references: UNIPROT:Q28473; EMBL:X15737; NID:G38047; PIDN:CAA33755.1; PID:993012  
C:Superfamily: apolipoprotein B

Query Match 100.0%; Score 44; DB 2; Length 596;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRKRGK 9

DB 227 RLTRKRGK 235



A:Accession: A25572  
 A:Molecule type: mRNA  
 A:Residues: 4219-4337, 'S', 4339-4563 <PFI>  
 A:Cross-references: GB:M3676  
 R:Wei, C.F.; Chen, S.H.; Yang, C.Y.; Marcel, Y.L.; Milne, R.W.; Li, W.H.; Sparrow, J.T.;  
 Proc. Natl. Acad. Sci. U.S.A. 82, 7265-7269, 1985  
 A:Reference number: A24738; PMID:86042646; PMID:2932736  
 A:Accession: A24738  
 A:Molecule type: mRNA  
 A:Residues: 'N', 3729-3731, 'I', 3733-3875, 'A', 3877-3948, 'F', 3950-3963, 'Y', 3965-3982, 'S', 39  
 A:Cross-references: GB:M2413; NID:9178735; PIDN:AA51742.1; PID:9178736  
 R:Chen, S.H.; Hahib, G.; Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silberman, S.R.; Cal  
 Science 238, 363-366, 1987  
 A:Title: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in  
 A:Reference number: A40133; PMID:88018019; PMID:3659919  
 A:Accession: B40133  
 A:Molecule type: mRNA  
 A:Residues: 2165-2179 <CHI>  
 A:Cross-references: GB:M18036; PIDN:AA51754.1; PID:9178800  
 A:Note: this mRNA includes the stop codon of the organ-specific mRNA for apo48  
 A:Accession: A40133  
 A:Molecule type: protein  
 A:Residues: 51-75; 101-110; 129-139; 158-174; 197-207; 276-287; 298-304; 306-314; 526-532; 538-55  
 36; 1486-1498; 1537-1556; 1563-1572; 1601-1610; 1647-1661; 1697-1724; 1770-1781; 1859-1897; 1968-  
 A:Note: these fragments were derived from apo48  
 R:Hardman, D.A.; Procter, A.A.; Schilling, J.W.; Kane, J.P.  
 Biochem. Biophys. Res. Commun. 149, 1214-1219, 1987  
 A:Title: Carboxyl terminal analysis of human B-48 protein confirms the novel mechanism f  
 A:Reference number: A28002; PMID:88105642; PMID:3426612  
 A:Accession: A28002  
 A:Molecule type: mRNA  
 A:Residues: 2129-2179, 2181-2235 <HA2>  
 A:Cross-references: GB:M18471  
 A:Experimental source: intestine  
 A:Note: this mRNA from intestine includes a stop codon created by RNA editing in place c  
 R:Mehrabian, M.; Schumaker, V.N.; Fareed, G.C.; West, R.; Johnson, D.F.; Kirchgessner, T  
 Nucleic Acids Res. 13, 6937-6953, 1985  
 A:Title: Human apolipoprotein B: identification of cDNA clones and characterization of t  
 A:Reference number: A24269; PMID:86041888; PMID:3903660  
 A:Accession: A24269  
 A:Molecule type: mRNA  
 A:Residues: 3056-3159 <MEH>  
 A:Cross-references: GB:X03045; NID:928783; PIDN:CAA26850.1; PID:929609  
 R:Hospatankar, A.V.; Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.B.  
 Biochem. Biophys. Res. Commun. 148, 279-285, 1987  
 A:Title: Identification of a novel in-frame translational stop codon in human intestine  
 A:Reference number: A29659; PMID:88049670; PMID:2445342  
 A:Accession: A29659  
 A:Molecule type: mRNA  
 A:Residues: 2169-2179 <HOS>  
 A:Note: the sequence shown represents the carboxyl end of apolipoprotein B-48  
 A:Note: two RNA species, 14.1kb and 7.5kb in length, were isolated from the human intest  
 ch encodes the 250K apoB-48, CAA encoding 2180-Gln is substituted by the stop codon TAA,  
 R:Yang, C.; Kim, T.W.; Weng, S.; Lee, B.; Yang, M.; Goto Jr., A.M.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 5523-5527, 1990  
 A:Title: Isolation and characterization of sulfhydryl and disulfide peptides of human ap  
 A:Reference number: A35783; PMID:90319144; PMID:2115173  
 A:Accession: A35783  
 A:Contents: disulfide bonds  
 A:Molecule type: protein  
 A:Residues: 28-41; 76-97, 'I', 99-100; 175-193; 206-215; 239-249; 259-266; 357-399; 455-490; 512-5  
 A:Note: cysteines at positions 112, 1422, 1505, 1662, 3761, 3917, and 4217 have free su  
 R:Lehoucq, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J.  
 FEBS Lett. 170, 105-108, 1984  
 A:Title: Human apolipoprotein B: partial amino acid sequence.  
 A:Reference number: A22006; PMID:84208786; PMID:6373369  
 A:Accession: A22006  
 A:Molecule type: protein  
 A:Residues: 873-892, 'K', 894-896 <LE1>  
 A:Accession: B22006  
 A:Molecule type: protein  
 A:Residues: 3113, 'L', 3115-3130, 'R', 3132-3133, 'P', 3135-3136, 'R' <LE2>

R:Blackhart, B.D.; Ludwig, E.M.; Pierotti, V.R.; Calati, L.; Onasch, M.A.; Wallis, S.C.;  
 U. Biol. Chem. 261, 15364-15367, 1986  
 A:Title: Structure of the human apolipoprotein B gene.  
 A:Reference number: A92564; PMID:87057153; PMID:2946672  
 A:Contents: annotation; gene structure  
 R:Wagener, R.; Pfitzner, R.; Stofel, W.  
 Biol. Chem. Hoppe-Seyler 368, 419-425, 1987  
 A:Title: Studies on the organization of the human apolipoprotein B 100 gene.  
 A:Reference number: A90715; PMID:87271140; PMID:2886136  
 A:Contents: annotation; gene structure  
 R:Weisgraber, K.H.; Rall Jr., S.C.  
 J. Biol. Chem. 262, 11097-11103, 1987  
 A:Title: Human apolipoprotein B-100 heparin-binding sites.  
 A:Reference number: A92605; PMID:87280197; PMID:3301850  
 A:Contents: annotation; heparin binding and disulfide bond  
 R:Daehli, N.; Lee, D.M.; Mok, T.  
 Biochem. Biophys. Res. Commun. 137, 493-499, 1986  
 A:Title: Apolipoprotein B is a calcium binding protein.  
 A:Reference number: A90125; PMID:86242245; PMID:3087360  
 A:Contents: annotation; calcium binding  
 R:Carlsson, P.; Olofsson, S.O.; Bondjers, G.; Darntof, C.; Wiklund, O.; Bjureell, G.  
 Nucleic Acids Res. 13, 8813-8826, 1985  
 A:Title: Molecular cloning of human apolipoprotein B cDNA.  
 A:Reference number: 137178; PMID:86093680; PMID:3841204  
 A:Accession: 137180  
 Query Match 100.0%; Score 44; DB 1; Length 4563;  
 Best Local Similarity 100.0%; Pred. No. 3.3;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RTRRRGLK 9  
 DB 3386 RTRRRGLK 3394  
 RESULT 5  
 apolipoprotein B-100 - rabbit (fragment)  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 31-Dec-1993 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
 C:Accession: A60950  
 R:Law, A.; Scott, J.  
 J. Lipid Res. 31, 1109-1120, 1990  
 A:Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL  
 A:Reference number: A60950; PMID:90324804; PMID:2373961  
 A:Accession: A60950  
 A:Molecule type: mRNA  
 A:Residues: 1-274 <LAW>  
 A:Cross-references: UNIPROT:Q7M2U9  
 A:Note: authors translated the codon GAT for residue 155 as His  
 C:Superfamily: apolipoprotein B  
 C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;  
 Query Match 88.6%; Score 39; DB 2; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 2.8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LTRRRGLK 9  
 DB 223 LTRRRGLK 230  
 RESULT 6  
 A60950  
 apolipoprotein B-100 - chicken (fragment)  
 C:Species: Gallus gallus (chicken)  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C:Accession: B60950  
 R:Law, A.; Scott, J.  
 J. Lipid Res. 31, 1109-1120, 1990  
 A:Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL  
 A:Reference number: A60950; PMID:90324804; PMID:2373961  
 A:Accession: B60950

A/Molecule type: mRNA  
A/Residues: 1-275 <LAW>  
A/Cross-references: UNIPROT:Q7L277  
C/Superfamily: apolipoprotein B  
C/Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;  
Query Match 88.6%; Score 39; DB 2; Length 275;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 223 LRRKRGK 9  
LRRKRGK 230  
RESULT 7  
UH0101  
apolipoprotein B-100 - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text\_change 09-Jul-2004  
C/Accession: JH0101; S3128; D60950  
R/Smith, T.J.; Hautamaa, D.; Maeda, N.  
Gene 87, 309-310, 1990  
A/Title: Sequence of the putative low-density lipoprotein receptor-binding regions of ap  
A/Reference number: JH0101; MUID:9026327; PMID:2332175  
C/Accession: JH0101  
A/Molecule type: DNA  
A/Residues: 1-784 <SMI>  
A/Cross-references: UNIPROT:Q61314; GB:M35186  
R/Smith, T.; Hautamaa, D.; Maeda, N.  
Submitted to the EMBL Data Library, May 1989  
A/Reference number: S31128  
A/Accession: S31128  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-531, 'S', 533-784 <SM2>  
A/Cross-references: EMBL:X15191  
R/Law, A.; Scott, J.  
J. Lipid Res. 31, 1109-1120, 1990  
A/Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL  
A/Reference number: A60950; MUID:90324804; PMID:2373961  
C/Accession: D60950  
A/Molecule type: mRNA  
A/Residues: 427-531, 'S', 533-700 <LAW>  
C/Genetics:  
A/Gene: MGI:Apob  
A/Cross-references: MGI:88052  
C/Superfamily: apolipoprotein B  
C/Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;  
F/435-445/Region: receptor binding  
F/646-656/Region: receptor binding  
Query Match 86.4%; Score 38; DB 2; Length 784;  
Best Local Similarity 88.9%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 648 LRRKRGK 9  
LRRKRGK 656  
RESULT 8  
AB1875  
hypothetical protein alr0547 [imported] - Nostoc sp. (strain PCC 7120)  
C/Species: Nostoc sp. PCC 7120  
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C/Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C/Accession: AB1875  
R/Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi,  
DNA Res. 8, 205-213, 2001  
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A/Reference number: AB1807; MUID:21595285; PMID:11758840

A/Accession: AB1875  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-680 <KUR>  
A/Cross-references: UNIPROT:Q8YZD0; GB:BA000019; PIDN:BA072505.1; PID:G17129892; GSPDB  
C/Genetics:  
A/Gene: alr0547  
C/Superfamily: hypothetical protein s111033; conserved hypothetical protein y100 homolo  
Query Match 84.1%; Score 37; DB 2; Length 680;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Db 544 RVTRRKG 9  
RVTRRKG 552  
RESULT 9  
A75334  
[acyl-carrier-protein] S-malonyltransferase (EC 2.3.1.39) DR1945 [similarity] - Deinococ  
C/Species: Deinococcus radiodurans  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C/Accession: A75334  
R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
'M.; Shen, M.; Vamathevan, J.; J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A/Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.  
A/Reference number: A75250; MUID:20036896; PMID:10567266  
C/Accession: A75334  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-305 <WHI>  
A/Cross-references: UNIPROT:Q9RT24; GB:AB002033; GB:AB000513; NID:G6459726; PIDN:AAF1149  
A/Experimental source: strain R1  
C/Genetics:  
A/Gene: DR1945  
A/Map position: 1  
C/Superfamily: [acyl-carrier-protein] S-malonyltransferase; [acyl-carrier-protein] S-mal.  
C/Keywords: acyltransferase; coenzyme A  
F/7-286/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>  
F/93/Active site: Ser (covalent substrate-binding) #status predicted  
F/198/Active site: His #status predicted  
Query Match 79.5%; Score 35; DB 2; Length 305;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 113 RVTRRKG 7  
RVTRRKG 119  
RESULT 10  
S34191  
sulfite reductase (NADPH2) (EC 1.8.1.2) hemoprotein - Thiocapsa roseopersicina  
C/Species: Thiocapsa roseopersicina  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-May-2004  
C/Accession: S34191  
R/Haverkamp, T.; Gisselmann, G.; Schwenn, J.D.  
Submitted to the EMBL Data Library, July 1993  
A/Description: Structure and function of genes involved in the metabolism of sulfite from  
A/Reference number: S34190  
C/Accession: S34191  
A/Molecule type: DNA  
A/Residues: 1-561 <HAV>  
A/Cross-references: EMBL:D23169  
C/Superfamily: sulfite reductase  
C/Keywords: 4Fe-4S; chromoprotein; cysteine biosynthesis; heme; iron; iron-sulfur protein  
F/423-429, 468, 472/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F/472/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 77.3%; Score 34; DB 1; Length 561;  
Best Local Similarity 87.5%; Pred. No. 54;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLTRKRGK 8  
|||  
Db 449 RLTRKRGK 456

## RESULT 11

salivary glue protein homolog precursor - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: S12607  
R:Putia, M.; Digilio, F.A.; Ariano, D.; Giordano, E.; Polito, L.C.  
Nucleic Acids Res. 18, 5837-5841, 1990  
A:Title: A new gene nested within the dance genetic unit of *Drosophila melanogaster*.  
A:Reference number: S12607; MUID:91016924; PMID:2120680  
A:Accession: S12607  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-107 <FUR>  
A:Cross-references: UNIPROT:P29338; GB:X52118; NID:g394803; PIDN:CAA36363.1; PID:g394804  
C:Genetics:  
A:Gene: FlyBase:ngl  
A:Cross-references: FlyBase:FBgn0002933  
A:Map position: 3C11-12  
C:Keywords: salivary gland; tandem repeat  
F:1-107/Domain: signal sequence #status predicted <SIG>  
F:31-62/Region: 8-residue repeats

Query Match 75.0%; Score 33; DB 2; Length 107;  
Best Local Similarity 55.6%; Pred. No. 20;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRKRGK 9  
|||  
Db 90 RLTRKRGK 98

## RESULT 12

salivary glue protein ng-2 - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S33822  
R:Putia, M.; Davino, P.P.; Crisp, S.; Attiaco, D.; Polito, L.C.  
J. Mol. Biol. 231, 531-538, 1993  
A:Title: Dense cluster of genes is located at the ecdysone-regulated 3C puff of *Drosophila*.  
A:Reference number: S33822; MUID:93287124; PMID:8510164  
A:Accession: S33822  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-112 <FUR>  
A:Cross-references: UNIPROT:P40139; EMBL:X61945; NID:g296040; PIDN:CAA43951.1; PID:g29604  
C:Genetics:  
A:Gene: FlyBase:ng2  
A:Cross-references: FlyBase:FBgn0010294

Query Match 75.0%; Score 33; DB 2; Length 112;  
Best Local Similarity 55.6%; Pred. No. 21;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRKRGK 9  
|||  
Db 90 RLTRKRGK 98

## RESULT 13

T41529

hypothetical protein SPCC645.12c - fission yeast (*Schizosaccharomyces pombe*)

C:Species: *Schizosaccharomyces pombe*  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T41529  
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.  
submitted to the EMBL Data Library, March 1999  
A:Reference number: Z22000  
A:Accession: T41529  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-198 <MOO>  
A:Cross-references: UNIPROT:Q9Y7V1; EMBL:AL049498; PIDN:CA339908.1; GSPDB:GN00068; SPDB:  
C:Genetics:  
A:Gene: SPDB:SPCC645.12c  
A:Map position: 3

Query Match 75.0%; Score 33; DB 2; Length 198;  
Best Local Similarity 77.8%; Pred. No. 34;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLTRKRGK 9  
|||  
Db 15 RLTRKRGK 23

## RESULT 14

B69407  
M0188 homolog - *Archaeoglobus fulgidus*  
N:Alternate names: inosine monophosphate dehydrogenase homolog [nismomer]  
C:Species: *Archaeoglobus fulgidus*  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: B69407  
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
J. Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
Glock, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Attiaco, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Weese, C.R.; Venter, J.C.  
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo-  
A:Reference number: B69250; MUID:98049343; PMID:9389475  
A:Accession: B69407  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-259 <KLE>  
A:Cross-references: UNIPROT:O29009; GB:AE001017; GB:AE000782; NID:g2689340; PIDN:AAB8998  
C:Superfamily: conserved hypothetical protein M0188; CBS homology  
F:12-60/Domain: CBS homology <CBS1>  
F:71-119/Domain: CBS homology <CBS2>

Query Match 75.0%; Score 33; DB 1; Length 259;  
Best Local Similarity 66.7%; Pred. No. 44;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLTRKRGK 9  
|||  
Db 227 RLTRKRGK 235

## RESULT 15

AH0906  
conserved hypothetical protein STY3508 [imported] - *Salmonella enterica* subsp. *enterica*.  
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh  
A>Note: this species has also been called *Salmonella typhi*  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AH0906  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,  
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Garra, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov-  
A:Reference number: AB0502; MUID:21534947; PMID:11677608

Thu Jan 13 09:04:59 2005

us-10-657-404a-8.rpr

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A/Accession: AH0906  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-309 <PAR>  
A/Cross-references: GB:AL513382; PDB:CMD07846.1; PTD:916504394; GSPDB:GN00176  
A/Genetics:  
A/Gene: STY3508  
A/Superfamily: Methanococcus jannaschii  
A/Supernamely: ?

Query Match	75.0%	Score 33;	DB 2;	Length 309;
Best Local Similarity	66.7%	Pred. No. 51;		
Matches	6;	Conservative	2;	Mismatches 1;

Qy	1	RLTRKGLK	9
		: :	
Db	171	RIARERGLK	179

Search completed: January 12, 2005, 13:31:58  
Job time : 17.5484 secs



RL Mol. Phylogenet. Evol. 28:225-240(2003).  
 DR EMBL; AY24379; AAP50767.1; -.  
 KW Lipoprotein.  
 FT NON\_TER  
 SQ SEQUENCE 421 421  
 1 1

Query Match 100.0%; Score 44; DB 2; Length 421;  
 Best Local Similarity 100.0%; Pred. No. 1.4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRKRGK 9  
 |||||  
 Db 265 RLTRKRGK 273

## RESULT 3

Q7YR10 PRELIMINARY; PRT; 432 AA.  
 AC Q7YR10; 01-OCT-2003 (TReMBLrel. 25, Created)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)  
 DE Apolipoprotein B (Fragment).  
 OS Dicerus bicornis (Black rhinoceros).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Diceros.  
 OX NCBI\_TaxID=9805;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=22761261; PubMed=12878460;  
 RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;  
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
 RL Mol. Phylogenet. Evol. 28:225-240(2003).  
 DR EMBL; AY24375; AAP50763.1; -.  
 KW Lipoprotein.  
 FT NON\_TER  
 SQ SEQUENCE 432 AA; 48171 MW; F27B7AB39604732C CRC64;

Query Match 100.0%; Score 44; DB 2; Length 432;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRKRGK 9  
 |||||  
 Db 276 RLTRKRGK 284

## RESULT 4

Q7YOM8 PRELIMINARY; PRT; 436 AA.  
 AC Q7YOM8; 01-OCT-2003 (TReMBLrel. 25, Created)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)  
 DE Apolipoprotein B 100 (Fragment).  
 OS Name=apob-100;  
 OS Nyctimene albigaster (Common tube-nosed fruit bat).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;  
 OC Pteropodidae; Nyctimene.  
 OX NCBI\_TaxID=48988;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=22761261; PubMed=12878460;  
 RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;  
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
 RL Mol. Phylogenet. Evol. 28:225-240(2003).  
 DR EMBL; AF548435; AAP97391.1; -.  
 KW Lipoprotein.

FT NON\_TER  
 SQ SEQUENCE 436 AA; 48717 MW; 1C4A7EAD72D2C629 CRC64;  
 1 1

Query Match 100.0%; Score 44; DB 2; Length 436;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRKRGK 9  
 |||||  
 Db 280 RLTRKRGK 288

## RESULT 5

Q7YOM7 PRELIMINARY; PRT; 438 AA.  
 AC Q7YOM7; 01-OCT-2003 (TReMBLrel. 25, Created)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)  
 DE Apolipoprotein B 100 (Fragment).  
 OS Name=apob-100;  
 OS Pteropus hypomelanus (Small flying fox).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;  
 OX NCBI\_TaxID=9405;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=22761261; PubMed=12878460;  
 RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;  
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
 RL Mol. Phylogenet. Evol. 28:225-240(2003).  
 DR EMBL; AF548436; AAP97392.1; -.  
 KW Lipoprotein.  
 FT NON\_TER  
 SQ SEQUENCE 438 AA; 48734 MW; 2BD85BCB4E2CC41 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 438;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRKRGK 9  
 |||||  
 Db 282 RLTRKRGK 290

## RESULT 6

Q7YR04 PRELIMINARY; PRT; 438 AA.  
 AC Q7YR04; 01-OCT-2003 (TReMBLrel. 25, Created)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)  
 DE Apolipoprotein B (Fragment).  
 OS Roussetus amplexicaudatus (Common rousette).  
 OS Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;  
 OC Pteropodidae; Roussetus.  
 OX NCBI\_TaxID=58083;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=22761261; PubMed=12878460;  
 RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;  
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling  
 RL Mol. Phylogenet. Evol. 28:225-240(2003).  
 DR EMBL; AY24383; AAP50771.1; -.  
 KW Lipoprotein.  
 FT NON\_TER  
 SQ SEQUENCE 438 AA; 48734 MW; 2BD85BCB4E2CC41 CRC64;

Qy 1 RLTRKRGK 9  
 |||||  
 Db 282 RLTRKRGK 290

SQ SEQUENCE 438 AA; 48597 MW; 41C890DEAF95C872 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 438;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RUTRRKGLK 9

DB 282 RUTRRKGLK 290

RESULT 7

ID Q7NR08 PRELIMINARY; PRT; 445 AA.

AC Q7NR08 01-OCT-2003 (TRENBLrel. 25, Created)

DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)

DE Apolipoprotein B (Fragment)

OS Chaetophractus villosus (South American armadillo)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Edentata; Dasypodidae; Chaetophractus.

NCBI\_TaxID=29080;

RP SEQUENCE FROM N.A.

RA MEDLINE=22761261; PubMed=12878460;

RT "A new phylogenetic marker, apolipoprotein B, provides compelling

RL Mol. Phylogenet. Evol. 28:225-240(2003).

DR EMBL; AY243378; AAP50766.1; -.

KM Lipoprotein.

FT NON\_TER 1 445

SQ SEQUENCE 445 AA; 49564 MW; 2DA5DC3ED2F0FDD2 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 445;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RUTRRKGLK 9

DB 289 RUTRRKGLK 297

RESULT 8

ID Q7TN64 PRELIMINARY; PRT; 445 AA.

AC Q7TN64 01-OCT-2003 (TRENBLrel. 25, Created)

DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)

DE Apolipoprotein B (Fragment)

OS Agouti paca (Paca)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Agoutidae; Agouti.

NCBI\_TaxID=108852;

RP SEQUENCE FROM N.A.

RA MEDLINE=22761261; PubMed=12878460;

RT "A new phylogenetic marker, apolipoprotein B, provides compelling

RL Mol. Phylogenet. Evol. 28:225-240(2003).

DR EMBL; AF548417; AAP97373.1; -.

KM Lipoprotein.

FT NON\_TER 1 445

SQ SEQUENCE 445 AA; 49721 MW; 34AF7ABE90F121EF CRC64;

Query Match 100.0%; Score 44; DB 2; Length 445;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RUTRRKGLK 9

DB 289 RUTRRKGLK 297

RESULT 9

ID Q7TN71 PRELIMINARY; PRT; 445 AA.

AC Q7TN71 01-OCT-2003 (TRENBLrel. 25, Created)

DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)

DE Apolipoprotein B (Fragment)

OS Hydrochaeris hydrochaeris (Capybara) (Carpincho)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Hydrochaeridae;

NCBI\_TaxID=10149;

RP SEQUENCE FROM N.A.

RA MEDLINE=22761261; PubMed=12878460;

RT "A new phylogenetic marker, apolipoprotein B, provides compelling

RL Mol. Phylogenet. Evol. 28:225-240(2003).

DR EMBL; AY243369; AAP50757.1; -.

DR InterPro; IPR000871; Beta\_lactamase\_A.

DR PROSITE; PS00146; BETA\_LACTAMASE\_A; UNKNOWN\_1.

KM Lipoprotein.

FT NON\_TER 1 445

SQ SEQUENCE 445 AA; 49520 MW; CBBADDS3D7A18D2 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 445;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RUTRRKGLK 9

DB 289 RUTRRKGLK 297

RESULT 10

ID Q7TN72 PRELIMINARY; PRT; 445 AA.

AC Q7TN72 01-OCT-2003 (TRENBLrel. 25, Created)

DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)

DE Apolipoprotein B (Fragment)

OS Erethizon dorsatum (North American porcupine)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Erethizontidae;

NCBI\_TaxID=34844;

RP SEQUENCE FROM N.A.

RA MEDLINE=22761261; PubMed=12878460;

RT "A new phylogenetic marker, apolipoprotein B, provides compelling

RL Mol. Phylogenet. Evol. 28:225-240(2003).

DR EMBL; AY243368; AAP50756.1; -.

KM Lipoprotein.

FT NON\_TER 1 445

SQ SEQUENCE 445 AA; 49617 MW; 9572FE5FE7625F2 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 445;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RUTRRGGLK 9  
Db 289 RUTRRGGLK 297

## RESULT 11

Q28473 ID Q28473 PRELIMINARY; PRT; 596 AA.  
AC Q28473; 289 RUTRRGGLK 297  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DE Apolipoprotein B (Fragment).  
OS Macaca fascicularis (Craab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA MEDLINE=92075708; PubMed=1742325;  
RA Page M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,  
RA Marotti K.R., Melchior G.W.,  
RT "Apo B metabolism in the cynomolgus monkey: evidence for post-  
RL transcriptional regulation.";  
RN Biochim. Biophys. Acta 1086:326-334(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Murray R.;  
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X15737; CAA33755.1; -.  
KW Lipoprotein.  
FT NON\_TER 1 1  
FT NON\_TER 596 596  
SQ SEQUENCE 596 AA; 66757 MW; B13BA74E25C3120 CRC64;  
Query Match 100.0%; Score 44; DB 2; Length 596;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 RUTRRGGLK 9  
Db 227 RUTRRGGLK 235

## RESULT 12

Q60536 ID Q60536 PRELIMINARY; PRT; 780 AA.  
AC Q60536;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DE Hamster apolipoprotein (apob) (Fragment).  
OS Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Mesocricetus.  
OX NCBI\_TaxID=10036;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90236327; PubMed=2332175;  
RA Smith T.J., Hautamaa D., Maeda N.;  
RT "Sequence of the putative low-density lipoprotein receptor-binding  
RL Gene 87:309-310(1990)."  
DR EMBL; M35187; AAA37059.1; -.  
DR PIR; C60950; C60950.  
DR PIR; JH0102; JH0102.  
KW Lipoprotein.

FT NON\_TER 1 1  
FT NON\_TER 780 780  
SQ SEQUENCE 780 AA; 86625 MW; E371D1B2079D8F7E CRC64;  
Query Match 100.0%; Score 44; DB 2; Length 780;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RUTRRGGLK 9  
Db 643 RUTRRGGLK 651

## RESULT 13

Q60537 ID Q60537 PRELIMINARY; PRT; 780 AA.  
AC Q60537;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DE Apolipoprotein B (Fragment).  
OS Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Mesocricetus.  
OX NCBI\_TaxID=10036;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Smith T., Hautamaa D., Maeda N.;  
RL Submitted (MAY-1989) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X15192; CAA33266.1; -.  
KW Lipoprotein.  
FT NON\_TER 1 1  
FT NON\_TER 780 780  
SQ SEQUENCE 780 AA; 86904 MW; 2D19CEA92170B6F9 CRC64;  
Query Match 100.0%; Score 44; DB 2; Length 780;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 RUTRRGGLK 9  
Db 643 RUTRRGGLK 651

## RESULT 14

Q13788 ID Q13788 PRELIMINARY; PRT; 3262 AA.  
AC Q13788;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DE APOB protein (Fragment).  
CN Name=APOB;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87191999; PubMed=2883086;  
RA Carlson P., Darnfor C., Olofsson S.O., Bjursell G.;  
RT "Analysis of the human apolipoprotein B gene; complete structure of  
RL the B-74 region.";  
DR EMBL; M15421; AAA51758.1; -.  
DR PIR; A27850; LPHUB.  
DR GO; GO:0005576; C:extracellular; NMS.  
DR GO; GO:0005319; F:lipid transporter activity; NMS.  
DR GO; GO:0006869; P:lipid transport; NMS.  
FT NON\_TER 1 1

SO SEQUENCE 3262 AA; 370140 MW; 56603BC0618DD40D CRC64;  
 Query Match 100.0%; Score 44; DB 2; Length 3262;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 RLTRKGLK 9  
 Db 2085 RLTRKGLK 2093

RESULT 15  
 APB\_HUMAN STANDARD; PRT; 4563 AA.  
 AC P04114; 000502; Q13787;  
 DT 01-NOV-1986 (Rel. 03, Created)  
 DT 01-NOV-1986 (Rel. 03, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein B-48 (Apo B-48)].  
 GN Name=APOB;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87016385; PubMed=3763409;  
 RA Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,  
 RA Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;  
 RT "Complete cDNA and derived protein sequence of human apolipoprotein B-100.";  
 RL Nucleic Acids Res. 14:7501-7503(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND VARIANT GLU-4181.  
 RX MEDLINE=88003974; PubMed=3652907;  
 RA Ludwig E.H., Blackhart B.D., Pierotti V.R., Caiati L., Fortier C.,  
 RA Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;  
 RT "DNA sequence of the human apolipoprotein B gene.";  
 RL DNA 6:363-372(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.  
 RX MEDLINE=87008488; PubMed=3759943;  
 RA Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,  
 RA Goto A.M., Jr., Chan L.;  
 RT "The complete cDNA and amino acid sequence of human apolipoprotein B-100.";  
 RL J. Biol. Chem. 261:12918-12921(1986).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87041416; PubMed=3464946;  
 RA Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,  
 RA Lee N., Brewer H.B., Jr.;  
 RT "Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino acid sequence.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87161758; PubMed=3030729;  
 RA Cladaras C., Hadjopoulos-Cladaras M., Nolte R.T., Atkinson D.,  
 RA Zannis V.I.;  
 RT "The complete sequence and structural analysis of human apolipoprotein B-100: relationship between apoB-100 and apoB-48 forms.";  
 RL EMBO J. 5:3495-3507(1986).  
 RN [6]  
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RP FUNCTION: Apolipoprotein B is a major protein constituent of  
CC chylomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apo  
CC B-100 functions as a recognition signal for the cellular binding  
CC and internalization of LDL particles by the apoB/E receptor.  
CC -!- SUBCELLULAR LOCATION: Secreted.

Db |||||  
3386 RLTRKRGK 3394

Search completed: January 12, 2005, 13:30:54  
Job time : 89.7097 secs

Query Match 100.0%; Score 44; DB 1; Length 4563;  
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RLTRKRGK 9